

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: embl-est58

Database:

1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2 6:em_est9 7:em_gss1 genbank-est111 1:gb_est1 11:gb_est12 12:gb_est13 13:gb_est1 11:gb_est12 12:gb_est13 13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17 17:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17 17:gb_est18 18:gb_est19 19:gb_est2 20:gb_est20 21:gb_est12 12:gb_est2 23:gb_est2 24:gb_est24 25:gb_est21 22:gb_est2 23:gb_est28 25:gb_est25 26:gb_est26 27:gb_est27 28:gb_est28 29:gb_est29 30:gb_est3 31:gb_est4 32:gb_est5 33:gb_est6 34:gb_est3 35:gb_est8 36:gb_est9 37:gb_gss1 38:gb_gss2 39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

Statistics: Mean 12.370; Variance 3.440; scale 3.596

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2.16e-24	2.16e-24	2.16e-24	2.16e-24	2.16e-24	2.16e-24	.16e-24	.16e-24	.16e-24	.16e-24	.46e-25	7.29e-24	7.29e-24	2.46e-25	7.29e-24	7.29e-24	7.29e-24	7.29e-24	2.46e-25	7.29e-24	8.29e-25	2.79e-25	8.29e-25	8.29e-25	.29e-25	.40e-25	.79e-25	.79e-25	.40e-25	.29e-25	.79e-25	.29e-25	.16e-25	3.16e-256	.16e-25

ALIGNMENTS

FEATURES E Source		JOURNAL C	TITLE C		SOURCE PORGANISM F	ACCESSION I	RESULT 1 LOCUS DEFINITION 1
High quality sequence stop: 340. Location/Qualifiers 1340 /organism="Homo sapiens"	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 2041 row: D column: 13	Sequencing Unpublished (1998)	wainairas, v. v., wailace, v. C., Smith, K., Swartzell, S., Furlong, J., Shaker, R., Schmidt, S., Traicoff, R. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 340)	GSS. human. Homo sapiens	Sequence. 903-91483 93655712 AQ230483.1 GI:3655712	AQ230483 340 bp DNA GSS 25-SEP-1998 HS_2041_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey

BASE C

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Matches

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FEATURES

source

COMMENT

JOURNAL TITLE REFERENCE

SOURCE KEYWORDS

ORGANISM

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
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CITBI-E1-2581D3.TF CITBI-E1
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Clones are available from Research Genetics (info@resgen.com).
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                                                             /organism="Homo sapiens"
/note="Vector: pBeloBAC11; Site_1: EcoRI;
CalTech Human BAC Library D"
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/clone="plate=2041 Col=13 Row=D"
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E-Coli DH108"
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                                                                                                                                                                               Email: hbe@tigr.org
For clone availability, please contact Pieter de Jong
For clone availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao, William Nies
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 556)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
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Other_GSSs: RPCI11-143N11.TJ
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Use of BAC End Sequences
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
/note="GDB:7554850"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="sperm"
114 c 86 g
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Pred. No. 4.98e-268;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                       William Nierman,
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144 TTGTTTTGTTTCAGACAGAGTTTCACTCTTGTTGCCCAAGCTGGAGTGCAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 CTGAGTAGCTGCGATTACAGGCATGCACCACCACGCCAGGCTAATTTTGTATTTTAATA 213
                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGGACCCGGGCC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gagatggggtttctccacgttggtcaggctggtcttgaactcccggccttagatgatcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bepler,G., O'Briant,K.C., Kim,Y.C., Schreiber,G. and Pitterle,D.M. A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOHILA metastasis suppressor
                                                                                                                                                                                                                                                                                                       Submitted (27-OCT-1998) Medicine and Radiology, Duke Medical Center, Box 2610, MSRB, Room 117, Durham, NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                Bepler, G., O'Briant, K.C., Kim, Y.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                      99134294
                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 55 (2), 164-175 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Similarity 85.5%;
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                                                                                                                        /clone="pTWB115.03T7"
/note="part of a 1.4 megabase contig including metastasis suppressor region Bin F" metastasis suppressor region Bin F" 224 c 177 g 260 t 37 others
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167 c 105 g 17
                                                                                                                                                                                                /map="11p15.5"
                                                                                                                                                                                                                    /chromosome="11"
                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone_lib="RPCI11"
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                                                      8.98;
85.38;
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                                   Pred.
                                                    Score 217; DB 42;
Pred. No. 1.19e-260;
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Pred. No. 3.56e-259;
0; Mismatches 43;
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11 clone pTWB115.03T7 map 11p15.5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: Donald Orlic, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA557945 325 bp mRNA EST 09-SEP-199/ ml17b07.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040917 similar to contains allu repetitive element;, mRNA sequence.
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced g1:1402126
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat
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Eutheria; Primates;
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quality sequence stop: 277.
    Location/Qualifiers
                      54
                   /db_xref="taxon:9606"
/clone="IMAGE:1040917"
/clone_lib="NCI_CGAP_HSC1"
/tissue_type="stem cells"
/lab_host="DH10B"
a 97 c 78 g 96 t
                                                                                                                                                                                                                                                 /Organism="Homo sapiens"
/note="Organ: bone marrow; Vector: pAMP10; mRNA made from flow-sorted CD34+/CD38- hematopoietic stem cells, cDNA made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp. CDNA Library Preparation: David B. Krizman, Ph.D. Poferorog.
                                                                                                                                                                                          DNA
                                                                                                                                                                                                         Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                 Center
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Unpublished (1997)
On May 18, 1998 th
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                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can b
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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253; Conser
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                             /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                               /clone="IMAGE:2224408"
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102 c 76 g
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Score 214; DB 29;
Pred. No. 3.16e-256;
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On Jan 24, 1995 this sequence version
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/note="Vector: pANPIO; mRNA made from liposarcoma, cDNA
/note="Vector: pANPIO; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                               56:5380-5383.
                                   /clone="IMAGE:1061719"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
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GGCCGGGCGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAAGGTCAAGGCTGGCGGA 96
                                                                                                                                                                                                                                                                                                               401 Queen Anne Avenue North, Seatt Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3023 row: N column: 20
Class: BAC ends
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HS_3023_B2_G10_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3023 Col=20 Row=N, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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                                  252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                     /sex="male"
102 c
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/clone="Plate=3023 Col=20 Row=N"
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                     GAGTTTTGCTCTTGTTGCCCAGGCTGGAGTGCAATGGTGCGATCTCGGCTCATTGCAACC 67
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Unpublished (1997)
On Jun 5, 1998 this
                                                                                  246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Life Technologies catalog #: 11548-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
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llarity 86.9%;
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                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Satie_2: Not1; Cloned unidirectionally. Primer: Oligo of Average insert size 1.72 kb. Life Technologies catalog 11548-013"
                                                                                                                                                                              /clone="IMAGE:2223057"
/clone=lib="NCI_CGAP_Pan1"
/tissue_type-"adenocarcinoma"
/lab_host="DH10B"
121 c 127 g 110 t
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                                                                             Score 215; DB 28;
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TCTTGGCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCT 326
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For clone availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
Research Genetics (info@resgen.com). BAC end search page:
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Department of Eukaryotic Genomics
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Use of BAC End Sequences from Library
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                       /cell_type="Lymphocytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD:
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Other_GSSs: RPCI11-151M17.TV
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Use of BAC End Sequences from Library
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/db_xref="GDB:7557904"
                                                                                                                                                                                                                                              /cell_type="Lymphocytes"
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                                                                    TCACTTGAGGTTGGGAGTTCGTGACCAGCCTGACCAACATGGAGAAGCCCCCGTCTCTACT 156
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/Organism="Homo sapiens"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
/db_xref="GDB:7553021"
                                                                                                                                                                                                                                                                         /cell_type="Lymphocytes"
175 c 185 g 16
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/clone="R-139B6"
                                                                                                                                                                                                                                                                                                             /sex="Male"
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Pred. No. 3.16e-256;
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2322 tcctgagtagccaggnttacagccatgcgctaccacgcccggctaatttngtatttnag
                                                                                                                                      2442 ttttttttttttttttggacagagttttgctcttgttaccccaggctggagtgcaatggc 2383
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                  303 TCCCAAGTAGCTAGGATTACAGGCATGCGCCACCCCTGGCTAATTTTGTATTTTTAG 362
                                                                                                                                                                      183 TITTITITITITITIGAGATGGGGTTTCACTCTCCTTGCCCAGGCTGGAGTGCAATGGT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: CITBI-E1-2527N10.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hbe@tigr.org
Clones are availabe from Research Genetics (info@resgen.com).
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ311398 762 bp DNA CITBI-E1-2527N10.TF CITBI-E1
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CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                /cell_type="sperm"
183 c 160 g
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Pred. No. 3.16e-256;
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                  174 TCACGAGTAGCTGGGATTACAGGCATGCGCCACCATGCCCGGCTAATTTTGTATTCTTAG
                                                                                                                   114 GCAATCTCGGCTCACCACAACTTCCACCTCCCAGGTTCAAGCAATTCTCTTGCCTCAGCC 173
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                                                                                                                                                                                                                                                            Match 8.7%;
Local Similarity 85.0%;
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earliens genomic clone Plate=3041 Col=3 Row=O, genomic surve
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Fax: (206) 616-3887
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: sperm; Vector: pBeloBAC11; E-Coli DH10B"
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Pred. No. 8.29e-252;
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                                                                              CTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGCTCGCGATGAGCTGAGATCGCGC 291
                                                                                                                                                                                                                                                                                                                                                            8.7%;
1 Similarity 84.5%;
251; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS_2198_A2_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col-20 Row-M, genomic survey
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HS_2198_A2_G10_MF_CIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
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John F. Collins, Biocomputing Research Unit.) 1993-1998 University of Edinburgh, U.K. ribution rights by Oxford Molecular Ltd a. database search, using Smith-Waterman algorithm an 18 15:44:26 2000; MasPar time 536.53 Seconds 975.257 Million cell updates/sec erated. 975.257 Million cell updates/sec erated. 975.257 Million cell updates/sec erated. 975.257 Million cell updates/sec 9246-129-1 42) from US09246129A.seq 10 cocaatcaagagaaattccaaggttttttttttttt

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Tumour necrosis facto
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SUMMARIES

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ALIGNMENTS

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Human c-fms oncogene.

c-fos gene.

Mutated BRCA1 genomic

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07-NOV-1994; WO-U12880.
21-NOV-1994; ZA-009229.
(HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A CDNA clone (730390), deposited as ATCC 75927, codes for tumour necrosis factor-gamma (R99453), a novel member of the TWF family. I was isolated from a human umbilical vein emotherlial cell cDNA library. The coding sequence can be incorporated into a vector and used for prodn. of recombinant TNF-gamma using bacterial, insect or mammalian cells as hosts. It may also be used as a diagnostic probe for gene mapping, or for the gene therapy of diseases involving abnormal cellular proliferation, e.g. tumours and cancer. Antisense sequences are useful as TNF-gamma antagonists.
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Use of interleukin-18 to inhibit osteoclast formation - in treatment of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma, chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism and osteoporosis Disclosure; Page 24-28; 56pp; English. Interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be used for interleukin-18 (II-18) or a functional equivalent can be use
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Pred.
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No. 9.84e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2114 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
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05-JUN-1998

(first entry)

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Query Match 9.2%;
Best Local Similarity 86.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a protein, which induces interferon-gamma (IFN-gamma) production in immunocompetent cells. The protein has high biological activity, including enhancing cytotoxicity of killer cells and inducing killer cell formation, in addition to inducing IFN-gamma production by immunocompetent cells when expressed in mammalian cells, facilitating its use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatments, minimising side effects. can be used in gene therapy, e.g. by the DNA or transplanting cells.
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                                                                                                                                                                                                                                                                                                             2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          low dosages to treat/prevent, e.g. malignant tumours, viral or bacterial infections and immune diseases. As it is expressed in mammalian cells, it also has low toxicity when used in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            malignant tumours or viral diseases
Claim 13; Pages 64-73; 74pp; Englis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic DNA encoding polypeptide inducing interferon-gamma production - by immuno-competent cells, useful to treat e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kurimoto M, Okura (
WPI; 98-054914/06.
P-PSDB; W47429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HAYB ) HAYASHIBARA SEIBUTSU
Kurimoto M, Okura T, Torigoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-1997; 304616.
27-JUN-1996; JP-185305.
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viral infection; bacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon-gamma; IFN-gamma; production inducer; gene therapy;
immunocompetent cell; treatment; prevention; malignant tumour;
viral infection; bacterial infection; immune disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA for interferon-gamma production inducer.
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atcacctgaagtcaggagttcaagaccagcctgaccaacatggaggaaaccccatctctac 23547
                                                                               gctgaggcaggagaatcttttgaacccgggaggcagaggttgcgatgagcctagatcgtg
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                                                                                                                                                                                                                          atcatctaaggccgggagttcaagaccagcctgaccaacgtggagaaaccccatctctac
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                                                                                                                                        tnaaaatacnaaattagccgggcgtggtagcgcatggctgtaancctggctactcaggag
                                                                                                                                                                                                                                                                                                                                                                                            258;
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28994 BP; 9141 A;
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15607..27049
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. No. 9.84e-124;
Mismatches 41;
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RESULT 5
ID V02032 standard; DNA; 40352
AC V02032;
DT 12-JUN-1998 (first entry)
DE MAGE-B cluster DNA sequence.
KW MAGE-B cluster DNA; testicul
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a fragment of the human thymopoletin gene, including exons 4 and 5. DNA encoding human thymopoletin, from a cDNA library prepared from human thymus RNA, may be expressed in a host cell e.g. bacterium (preferably Escherichia coll), fungus, insect or mammalian cell for production of recombinant thymopoletin has a regulatory effect on the mammalian immune system, and can be used for treating/modulating an immune or nervous system condition, and for the treatment of chronic infection, autoimmune disorders and certain affective psychiatric or neurological disorders. The protein and the DNA can be used as diagnostics; the DNA can be used in gene therapy.

Sequence 6905 BP; 2028 A; 1280 C; 1359 G; 2238 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIMMU-) Immunution G, Harris C
Culler MD, Goldstein G, Harris C
Shenbagamurthi P, Siekierka JJ, ?
WPI; 95-240474/31.
Polynucleotide(s) encoding human
Polynucleotide(s) encoding human
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09-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92779 standard;
                                                                                                                                                                                                                                                                                       2205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system conditions.
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29-JUN-1995.
13-DEC-1994; U14356.
21-DEC-1993; US-171382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isclosure; Fig 9a-9g; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                    ctgaggcaggagaatcgcttgaaccttggaggcggaggttgctgtgagccgagatcgcgc 6410
                                                                                                                                                                                                                                                                                                    tcacctgaggtccggagttcgagacgagcctgaccaacatggagaaaccctgtctctact 6290
                                                                                                                                                                                                                                                                                                                                          ccgaggcagaanaattncttgaactggggaggcagaggttgcggtgagcccagancgcgc
                                                                                                                                                                                                                               naaaatacnaaattagccgggcgtggtagcgcatggctgtaancctggctactcaggagg
                                                                                                                                                                                                                                                                                     tcatctaaggccgggagttcaagaccagcctgaccaacgtggagaaaccccatctctact
                                                                                                                                                                                                                                                                                                                                                                                                              h 8.8%;
Similarity 84.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
  DNA sequence.
DNA; testicular
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/note= "exon 5"
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4691.4788
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ka JJ, Talle
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1280 C;
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Pred.
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     seminoma; cancer; screening; leukaemia
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W09746710-A1.
11-DEC-1997.
05-JUN-1997; U09774.
25-APR-1997; US-846111
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                               polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                          carcinoma;
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29748..31827
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31475..
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31403..3
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35140.
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23546..25194
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23607..24647
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7961..7966
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Best Local Similarity 85.1%;
Matches 258; Conservative
WO9709421-A1.
13-MAR-1997.
06-SEP-1995; U13816.
08-SEP-1995; US-525058.
(UNMI ) UNIV MICHIGAN.
Legault DJ, Lowe JB;
                                                                                                                                                                                                                                                                                                                                 T61677 standard; DNA; 8174 BP.
T61677;
19-JUN-1997 (first entry)
Human alpha(1,2)-fucosyltransferase DNA.
Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide; blood group H; ss.
                                                                                                                                                                                                                                                                                                                       Homo
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(LUDW-) LUDWIG INST CANCER RES.
BOON T, Brasseur F, Lurquin C;
WPI; 98-042216/04
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Pred. No. 9.21e-118;
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Best Local
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Example 1; Page 274-279; 329pp; English.

A DNA sequence (T61677) codes for human GDP-Fuc:beta-D-
galactoside alpha(1,2)-fucosyltransferase (W13640), an enzyme
involved in the expression of type I and II blood group H
structures. It was obtd. by transfecting mouse L cells with DNA
derived from human A431 cells, and selection of transfectants the
expressed the H antigen by using anti-H antibody in a panning
procedure. The DNA can be used to construct animal cell lines
with specific capabilities with respect to post-translational
modification of the oligosaccharides of expressed proteins or
                                                                                                                                                                                                                                           22-AUG-1991;
14-FEB-1991;
14-FEB-1990;
14-FEB-1990;
12-DEC-1990;
            e.g. the presence of soluble or membrane bound oligo or polysaccharide or glycosyltransferase. pisclosure; Fig 3; 155pp; English.

The DNA encodes a protein sequence capable of functioning as a gdp- ruc:[beta-p-Gal alpha(1,2)- fucosyltransferase. The sequence coded by nucleotides 4782 - 5780 represents the functional protein the enzyme produced by the DNA sequence can be used in enzymatic fucosylation of chain-terminating galactose residues on lactose-
                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1991 (first entry) GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase Glycosyltransferase.
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                                                                                                                                                                          P-PSDB; R13751.
                                                                                                                                                                                        Lowe JB;.
WPI; 91-267151/36.
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                                                                                                                                                      Isolation of gene conveying post-translational characteristic
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1 Similarity 84.8%;
251; Conservation
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8174 BP;
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US-480133.
US-479858.
US-627621.
V OF MICHIGAN.
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   type
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Pred. No. 1.95e-116;
0; Mismatches 45;
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                                                                                                                                                                                                                                                                    DNA fragment encoding a glycosyltransferase - can be used for in vitro reactions to modify cell surface oligosaccharide(s) e.g. blood gp. determinants to protect against transplant rejection pisclosure; Fig 3; 249pp; English.

The sequence is that encoding human glycosyl transferase. The enzyme produced by the DNA may be non glycosylated. This prevents premature loss of enzyme activity. It can also be used in in vitro reactions to modify cell surface oligosaccharide mols. e.g. blood group determinants. See also 056905-12.

See also 056905-12.

See also 056905-12.

1628 A; 2228 C; 2322 G; 1996 T;
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20-JUL-1992; US-914281
(UNMI ) UNIV MICHIGAN.
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ctgagtagccaggnttacagccatgcgctaccacgcccggctaatttngtatttnagta
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Similarity 84.8%;
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Pred. No. 1.95e-116;
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Pred. No. 1.95e-116;
Pred. Tartches 45;
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V57272;
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RESULT 10
ID T94101 standard; DNA; 53526 BP
AC T94101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC isolated from a bacterial artificial chromosome (BAC) library covering Ct the complete human genome. Clone BAC 123H04M was isolated using STS C probes and markers based on human chromosome 1 (the gene's location CC was confirmed as being in the region 1q23-q25 by fluorescence in situ hybridisation). The BAC clone was digested with restriction enzymes. The fragments were subcloned and the inserts sequenced. The human FMO Sequence was identified by homology to known FMO sequences. Fragments CC of the FMO2 sequence can be used as primers or probes specific for CC particular alleles, especially the G.125 anac. A mutation. Detection of this mutation allows diagnosis of a predisposition to FMO-associated CC diseases, particularly juvenile wide-angle primary glaucoma (WAPG), CC but more generally any condition involving altered response to cxidative stress, including toxic and degenerative disorders, coidative stress, including toxic and degenerative disorders are excessive or inadequate CC degeneration. Other FMO-related disorders are excessive or inadequate CC degeneration of drugs, toxic xenobiotics or carcinogens. The process and cells expressing them can also be used for the biosynthesis/biodegradation, particularly detoxification, of xenobiotics of pharmaceuticals, food additives, pesticides and herbicides. Sequence 26016 BP; 8046 A; 5211 C; 5049 G; 7710 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.6%;
Best Local Similarity 84.2%;
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Claim 2; Page 49-65; 163pp; French.
Claim 2; Page 49-65; 163pp; French.
This sequence represents the genomic clone encoding the human flavin-containing mono-oxygeness isoform 2 (hFMO2). The sequence of the seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding iso-forms 2 and x of human flavin-containing mono-oxygenase - useful for diagnosis, treatment and prevention of e.g. wide-angle primary glaucoma and for synthesis and degradation
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05-DEC-1997; F02226.
06-DEC-1996; FR-015032.
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WPI; 98-333333/29.
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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24484..25486
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Pred. No. 1.89e-114;
0; Mismatches 47; Indels 0;
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Matches 26
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22-MAY-1997; U08799.
23-JUN-1996; US-658136.
24-MAY-1996; US-655360.
(GENZ) GENZYME CORP.
Burn T, Connors T, Dackov
27-NOV-1997.
22-MAY-1997; U08799.
23-JUN-1996; US-658136.
24-MAY-1996; US-655360.
(GENZ) GENZYME CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose human autosomal or adult onset polycystic kidney disease claim 2; Pages 90-118; 257pp; English.

The present sequence is the human polycystic kidney disease 1 (PKD1) gene. The PKD1 gene or polypeptide may be used to treat autosomal dominant polycystic kidney disease (APKD), and identify carriers of mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies (Ab) that distinguish between normal and mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 Ab may also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. Ab are also useful in rational drug design studies to identify and test inhibitors of
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Qian
WPI;
                                                                                                      Human PKD1 locus between chromosomal markers ATPL (ATP6C) Human; polycystic kidney disease 1; PKD1; treatment; autosomal dominant polycystic kidney disease; APKD; ss.
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used
                                                                           Homo sapiens. W09744457-A1.
                                                                                                                                                                     T94108 standard; DNA; 53577 T94108;
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mal dominant polycystic kidney disease; APKD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.6%;
Similarity 82.1%;
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8486 A;
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Pred. No. 4.12e-115;
0; Mismatches 57;
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The present sequence is the human polycystic kidney disease 1 (PKDI) locus between chromosomal markers ATPL (ATPBC) and D16884.

The PKDI gene or polypeptide may be used to treat autosomal disease (AFKD), and identify carriers of mutant PKDI genes, i.e. subjects susceptible to APKD. Antibodies (Ab) that distinguish between normal and mutant PKDI sequences can also be used in diagnostic tests. Anti-PKDI amay also be used to perform subcellular and histochemical localisation studies, and to block the function of PKDI. Ab are also useful in rational drug design studies to identify and test inhibitors of PKDI. Sense and antisense sequences derived from the PKDI gene may used for detection and therapy.

Sequence 53577 BP; 8495 A; 17684 C; 15782 G; 11616 T;
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Best Local S
Matches 26
                                                                                                                                                                                                                                                                        06-MAY-1997 (first entry)
06-MAY-1997 (first entry)
Human polycystic kidney disease normal PKD1 gene.
Adult onset polycystic kidney disease; APKD; autosomal mutant; transversion; transition; deletion; insertion;
                                                                                                               old_sequence
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Qian F;
WPI; 98-018511/02.
 W09612033-A1
25-APR-1996.
                                                                 old_sequence
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1 Similarity 82.1%;
261; Conservation
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                                              /note- "replaces Val
insert(51827..51828,
/*tag= d
                                                                                                                                                             /note- "specifically claimed region cDNA identified by exon trapping" replace(50652..50653, cg)
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                                                                                                               /note= "changes Val codon replace(50796..50797, cg)
                              "insertion, results
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Pred. No. 4.12e-115;
0; Mismatches 57;
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polycystic kidney disease
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SQ Sequence 53577 BP; 8495 A; 17681 C; 15785 G; 11616 T;
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12-OCT-1994; US-323443.
31-UAN-1995; US-381520.
(IGIG-) IG LAB INC.
(UYJO) UNIV JOHNS HOPKINS.
      WO9846757-A2
22-OCT-1998.
                                                                                      mat_peptide
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V62746 standard; cDNA;
V62746;
15-FEB-1999 (first ent
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WPI; 96
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Similarity 82.1%;
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2249..2287
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Pred. No. 4.12e-115;
0; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PT New polynucleotide(s) encoding secreted human proteins - are derived PT from, e.g. human foetal brain or foetal kidney cDNA libraries, PT potentially useful as, e.g. vaccines or thrombolytic agents Claim 1; Page 67-68; 120pp; English.

CC contain 1; Page 67-89; 120pp; English.

CC secreted protein (see W74720). It was isolated from a human foetal brain cDNA library using methods which are selective for cDNAs Contain cDNA; Library using methods which are selective for cDNAs Contain cDNA; Library using methods which are selective for cDNAs contain contain secreted proteins, or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. It shows some celement. The invention provides polynucleotides (see V62746-55) contain a claim train, adult testis, adult brain, adult kidney and foetal brain, adult testis, adult brain, adult kidney and foetal kidney (all deposited as composite clone ATCC 98404), which can contain a secreted proteins (see W74720-29). The polynucleotides and proteins are predicted to have blological activities which would conditions in humans and animals, although no supporting data are conditions in humans and animals, although no supporting data are conditions in humans and animals, although no supporting data are conditions in humans and animals, although no supporting data are conditions in humans and animals, although no supporting data are conditions and thrombolytic activity, tissue growth activity, hammune cativity, chemotactic/chemokinetic activity, catherin/tumour invasion suppressor activity, and tumour inhibition activity, The polynucleotides are cativity, and tumour inhibition activity, and can be used in recombinant production of the polypeptidess.

Sequence 2754 BP; 608 A; 671 C; 637 G; 838 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                           Hereditary haemochromatosis subregion from an HH affected individual. Bovine butyrophilin; BF; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism, NPT3; NPT4; RoRet; BTF1; BTP3; BTP3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia
type 1 sodium transport gene; Homo sapiens. W09814466-A1.
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                                                                                                                                                          21-DEC-1998 (first entry)
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13-APR-1998; US-059487.
15-APR-1997; US-843374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Racie LA, Spaulding V, Treacy M;
WPI; 98-568731/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agostino MJ, Jacobs K, LaVallie ER,
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                                                                                                                                                                                                     standard; DNA; 237326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250;
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Similarity 83.9%;
250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 208; DB 53;
Pred. No. 8.69e-114;
0; Mismatches 48;
                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 48;
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                                                                hypophosphatemia
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PS Claim 1; Fig 9; 209pp; English.

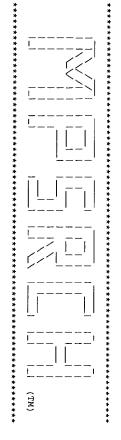
CC The present invention describes hereditary haemochromatosis gene. The present sequence converges of the present of the present of the common hereditary converges of the common hereditary converges of the presence or absence of the individual comprising:

CC (a) providing DNA or RNA from the individual; and (b) assessing the color of the presence or absence of absence of a haplotype or genotype where converges of the HFE gene mutation in the genome of the individual. The common sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present convertion also describes BTF genes, which are homologues of the milk convertion also describes BTF genes, which are homologues of the milk convertion and sequences from the products for the production of agonists converted by the convertion and sequences of the milk convertion and sequences of a type 1 sodium transport gene, and can be used for hypophosphatemia.

SQ Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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30-SEP-1997; U17658.
07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feder JN, Kronmal GS, La
Tsuchihashi Z, Wolff RK;
                                                                                                     Lecithin-cholesterol acytransferase-like gene.
Human; lecithin-cholesterol acyltransferase-like protein;
Human; agonist; arteriosclerosis; atherosclerosis; hyperlipidemia;
atherosclerosis hypercalorism; obesisty; hypertriglyceridemia;
inflammatory disease; senescence; renal disorder; Inhibition;
malnutrition; abetalipoproteinemia; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2382
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for the diagnosis and treatment c
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                                       Homo sapiens.
WO9846767-A1.
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                                                                                 Tangier disease;
                                                                                                                                                                                                                                                                     V68599 standard;
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                                                                                                                                                                                                                                                      v68599;
                                                                                                                                                                                                                                                                                                                                                           cacccaccttggcctcccaaagtgttgggattacaggtgtgagccactgcgcctggcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 8.5%;
Similarity 83.6%;
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                                                                                                                                                                                                                                                                          cDNA; 2867 BP.
                                                                                   ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 207; DB 50; 1
Pred. No. 3.99e-113;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e products - used to deve
of hereditary disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 237326;
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ders in iron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence encoding a novel human lecithin-cholesterol acyltransferase-like protein, used in the method of the invention. The novel proteins have LCAT-like activity. The proteins and agonists can be used for treating or preventing e.g. arteriosclerosis, atherosclerosis, hyperilipidemia, atherosclerosis hypercalorism, obesity, hypertriglyceridemia, inflammatory diseases, senescence, diseases of the brain, or renal disorder. Inhibitors of the protein can be used for treating or preventing e.g. malnutrition, the protein can be used for treating or preventing e.g. malnutrition.
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        2385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abetalipoproteinemia, inflammatory diseases, Tangier disease (analphalipoproteinemia) and other diseases. The products can also be used for detection, diagnosis and drug screening as part of a kit. Sequence 2867 BP; 660 A; 750 C; 905 G; 552 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated lecithin-cholesterol acyl:transferase proteins - used develop products for treating e.g. atherosclerosis, obesity, inflammatory diseases, senescence, diseases of the brain or remains of the brain of the brai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND Taniyama Y;
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11-APR-1997; JP-093355.
10-JUL-1997; JP-184885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1412 tcacctgaggttgcgagttcaagaccagcctgactaacatggagaaaaccccgtctctact 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 8.4%;
Local Similarity 84.2%;
ctgaggcaggagaattgcttgaatccaggagacggaggttacggtgagccaagattgcac
                                                                                                                                                                                                                                                                                                                                                                   aaaaatacaaaattagccagg-gtggtggcgcatgcctgcaatcccagctactcgggagg 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   naaaatacnaaattagccgggcgtggtagcgcatggctgtaancctggctactcaggagg 2324
                                                                                                                                                              ccgaggcagaanaattncttgaactggggaggcagaggttgcggtgagcccagancgcgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pages 152-154; 190pp; English
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Pred. No. 8.40e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Search completed: Tue Jan 18 15:54:43 2000 Job time : 617 secs.



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MPsrch_nn Run on: n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Jan 18 13:18:32 2000; MasPar time 4426.77 Seconds 1529.106 Million cell updates/sec

Description: Perfect Score: Title: >US-09-246-129-1 (1-2442) from US09246129A.seq 2436

N.A. Sequence: Comp:

Scoring table: TABLE default Gap 6

Nmatch

STD

Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: emb158

1:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_ln 8:em_com 9:em_cor 10:em_cv 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
genbanklll 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_com 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 11.877; Variance 6.071; scale 1.957

Statistics:

SUMMARIES

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13	12	11	10	9	8	7	σ	υı	4	w	N	ы	ult No.
223	224	223	226	226	226	229	232	231	232	231	231	2393	Score
	9.2	9.2	9.3	9.3	9.3	9.4	9.5	9.5	9.5	9.5	9.5	98.2	Query Match
105984	85285	76727	160258	145871	96115	40926	185371	180283	170820	123004	95855	2785	Query Match Length DB
19	19	29	19	29	20	29	29	31	20	29	30	31	BB
AC005087	HS469D22	HS821D11	HS500L14	HS302D9	AC006968	HSB10B1	HS625H18	AF134726	AC006286	HS196E23	HSAC000115	AF039390	ID
sapiens clone		Human DNA sequence fro	sequence	Human DNA sequence fro	Homo sapiens clone DJ0	Human DNA sequence fro	Human DNA sequence fro	Homo sapiens BAC clone	Homo sapiens, clone hR	Human DNA sequence fro	Human BAC clone GS188P	Homo sapiens vascular	Description
9.48e-147	1.48e-147	9.48e-147	3.60e-149		3.60e-149	1.36e-151	5.14e-154	3.30e-153	5.14e-154	3.30e-153	3.30e-153	0.00e+00	Pred. No.

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	<u>;</u> ;					2222	
149200 151691 227571 233421	143623 145528	126462 129541 131078 132323	43368 82976 82976 124351	236281 317311 333303 39441	145616 163847 177540 178109 195550	131078 133060 135630 135815	551 568 568 568 568
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quence *** quence *** clone RG3 Chromosom	lone	clone DJO 6 PAC clone 6 basic tra 6 juence ***	clone UWG 6 P1 clone 6 P1 clone 3 Xp22 bins 6	Xp22-132- , WORKING chromosom chromosom	DNA sequence fro sapiens clone DJO sapiens chromosom sapiens chromosom sapiens clone NHO	Homo sapiens basic tra 9 Homo sapiens clone DJ0 9 Human DNA sequence *** 9 Human DNA sequence *** 1	12q24 BAC DNA seque quence fro clone RG2 some 12p15
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ALIGNMENTS

	CDS	gene		source	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE	JOURNAL		TITLE			AUTHORS	XEF EXPINCE			ORGANISM	SOURCE	KEYWORDS	VERSION	NID	ACCESSION	C	LOCUS	RESULT 1
/gene- vBol /codon_start=1 /product="vascular endothelial cell growth inhibitor" /protein_id="AAD08783.1"	/gene="VEGI" 1124 . 1648 /cono-"VEGI"	/tissue_type="vascular endothelial" 12785	/organism="Homo sapiens"	12785	Location/Oualifiers	Submitted (19-DEC-1997) Human Genome Sciences, 9410 Key West Ave.,	Direct Submission	Yu,GL.	2 (bases 1 to 2785)	Unpublished	Angiogenesis	A Novel-Endothelial Cell-Specific Negative Regulator of	and Yu.GL.	Gentz,S., Lippman,M.E., Aggarwal,B.B., Ruben,S., Gentz,R., LillY.	ru, GL., Zhai, r., Ni, J., Iruela-Arispe, L., Huang, WQ., Xing, L.,	t (bases t to 2/63)	Primates; Catarrhini; Hominidae; Homo.	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	Homo sapiens	human.		AF039390.1 GI:4038080	94038080	AF039390	mRNA, partial cds.	7/85 pp	

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                                                                    ATAGGGGGATICCTTAACCTICATTGTTCTCCAGGATCATAGGTCTCAGGTAAAATTAAA 939
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1978	agatatctaaataaggaagtttgagtttcacatgtatatcccaaatacaacagttgct	1919	Qy
	AGATATCTAAATAAGGAAGTATGAGTTTCACATGTATATCAAAAATACAACAGTTGCTT	G	Дb
1918	ttggttttcatgtcatctacagcatatgagaaaagctacctttcttt	1859	Qy
2258	TIGGTTTTCATGTCATCTACAGCATATGAGAAAAGCTACCTTTCTTT	2199	Db
1858	cttgcctaaaaaaatgaaaagagagttggtatgtctcatg	1799	Qy
2198	TTGCCTAAAAAAAATGAAAAGAGAGTTGGTATGTCTCATGAATGTTCACACACA	2139	Дb
1798	aaaacagtataaactttcagaggcaaaatccttcaccaatttttccacatactt	1739	Qy
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2078	TGATCATAAATTTGCTTCAATTCAGGAGCTTTGAAGGAAG	2019	Дb
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2018	GAGAAATATTTCAACACCTCC-TGCTATACAATGGTCACCAGTGGTCCAGTTATTGTTC	1960	뮍
1618	actgatcactaaatgaatggatgatctactco	1559	Qy
1959	TAAATATTAAGACACTGATCACTAAATGAATGGATGATCTACTCGGGTCAGGATTGAA	1900	Дb
1558	agagagcaaatatattattaagatgggttggaggattggcgagtt	1499	Qy
1899	GGAAAAAGGCTGAAGAGAGAGAATATATTATTAAGATGGGTTGGAGGATTGGCGAG	1840	ф
1498	tttcacacttcatgtgccttactgatgagagta	1439	ργ
1839	CTATGAAATTTGGGGCCAAAATTTCACACTTCATGTGCCTTACTGATGAGAGTAC	1780	Дb
1438	ataaccaggggtttcttggggccgggagtagggggcattc	1379	Qy
1779	AACCAGGGGTTTTCTTGGGGCCGGGAGTAGGGGCATTCCACAGGGACAACG	1720	ДĎ
1378	tatcattatatgaaagtcc	1319	Qy
1719	CATTATATGAAAGTCCTCTGCCACCGAGTTCCTAATTTTCTTTGTTCAAATC	1660	ДЬ
1318	ttacacaaaagaagataaaaccttctttggagccttcttactataggaggagagc	1259	Qy
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1258	tcagtgacatctcttg	1199	Qy
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1198	ctggttccagcccatctacctcggag	1139	Qy
1539	GGGACCAAGTCTGTATGCGAAGTAGGTAGCAACTGGTTCCAGCCCATCTACCTCGGAGC	1480	рь
1138	ctaccctgagccaacccagctcctcat	1079	Qy
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ω	AAATTCCTGCTGATCCCAGAGTCGGGAGACTACTTCATTTACTCCCAGGTCACATTCC	1300	ДD
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1299	CTGCACTGGGAACATGAACTAGGCCTGGCCTTCACCAAGAACCGAATGAACTATACCAA	1240	Д

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGCTTGAACTGGGGAGGCAGAGGTTGCGGTGAGCCCAGATCGCGCCATTGCACTCCAGC
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                                                                                                 all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
           This clone is from Genome Systems Cell line: lymphoblastoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tin-Wollam,A, Graves,T and Ozersky,P.
The sequence of H. sapiens BAC clone GS188P18
Unpublished (1997)
Haplotypes:
                                                     SOURCE INFORMATION:
                                                                                       confirmed by restriction digest.
                                                                                                                                                                         This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                               neighboring submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                        Department of Genetics, Washington University St. Louis, MO 63108, USA http://genome.wustl.edu/gsce-e-mail: sapiens@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The location of this clone is unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEIGHBORING SEQUENCE INFORMATION:
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                                                                           complement(20761.
/rpt_family="L1"
22119 22393
                                                                                                                                                                                                                                                                                                                           /protein_id="AAB46354.1"
/db_xref="pl0:q1809231"
/db_xref="gl0:q1809231"
/db_xref="gl1:1809231"
/db_xref="gl1:1809231"
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NLHVPGPMAVKQFSPSLARRASVRPGELWHESSLAGTSSLEPGYSHPFPARHLVPEPQ
NLHVPGPMAVKQFSPSLARRASVRPGELWHESSLAGTSSLEPGYSHPFPARHLVPEPQ
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1365. .1658
                                                                                                                                    /rpt_family="ALU"
complement(16190.
/rpt_family="ALU"
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                    complement(23191. .23226)
/gene="WUGSC:H_GS188P18.1a"
                                                                                                                                                                                                                                                                                            PDGKREPLLSLLQQDRCLARPQESAARENGNPGQIAGSTGLLFNLPPGSVHYKKLYVS
RGSASTSLPNETLSELETPGKYSLTPPNHWGHPHRYLQHL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(14642. .14855,27209. .27628,29388. .29441,35071.

/gene="WUGSC:H_GS18818.1a"

/note="coded for by human cDNAs R76043 (NID:g850725),

R65857 (NID:g838495) and H12868 (NID:g877688)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(13000. .13356)
/rpt_family="L1"
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/rpt_family="L1"
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complement(6747.
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'note="GRAIL prediction, score =
                                                        /rpt_family="ALU"
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14642. .35159
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7948. .8236
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/clone="GS188P18"
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complement(37269. .39221)
/rpt_family="L1"
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42559.
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/rpt_family="L1"
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complement(31938. .32231)
/rpt_family="ALU"
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/rpt_family="ALU"
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/rpt_family="ALU"
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47263.
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GHPHRYLQHL"
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/gene="WUGSC:H_GS188P18.1b"
/note="GRAIL prediction, score =
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complement(31760.
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join(29366. .29441,35071. .35159)
/gene="WUGSC:H_GS188P18.1b"
complement (58296.
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/note="match to Human EST R28570 (NID:g784705)"
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/db_xref="GI:1809232"
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/rpt_family="MER"
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/rpt_family="ALU"
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2875 CTGGGCTGGGCGCAGTGGCTCACTCCTGTAATCCCAGCACTTTGGGAAGCCAAGGCGGGC 2934
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Submitted (02-JAN-1998) Chromosome X Project Group (http://www.sanger.ac.uk/HGP/ChrX/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 25, 1998 this sequence version replaced gi:2465037. IMPORTANT: This sequence is the entire insert of clone 196E23. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS196E23 123004 bp DNA PRI 18-JAN-1998 Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for the company of the contains of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 123004)
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69097. .69116
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/note="GRAIL prediction,
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pred. No. 3.30e-153;
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The true left end of clone 196E23 is at 1 in this sequence. The true right end of clone 196E23 is at 123004.

196E23 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.

Location/Qualifiers
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/note="MER43 repeat: matches 272. 10878. .11673
                                           /note="L1PA16 repeat: matches 271. .904 of consensus" 10317. .10577
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/note="AluJo repeat: matches 17.
                                                                                                            note="MIR repeat:
                                                                                                                                                                                                        /note="MLT1D repeat: matches 1. .505 of consensus"
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'note="AluSx repeat: matches 3. .283 of consensus;
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3991. .4177
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/clone="196E23"
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                                                             /note="2 copies of 136 mer 95 % 24111. .24152
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fsralsnikspqeltpssgsegvmlknddsmspnqwrysspwtkpqpevpvtnraanc
nlhvpgpmavnqfspslarrasvrpgelwhfsslagtsslepgyshpfparhlvpepq
pdgkrepllsllqqdrclarpqesaarengnpgqiagstgllfnlppgsvhykklyvs
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complement(17707. .42347)
/gene="dJ196E23.1"
17716. .17964
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38280. .38518,42218. .>42347))
/gene="dJ196E23.1"
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complement(join(17975. .18063,23693. .23768))
/gene="dJ196E23.1"
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complement(join(<17803. .18063,23693.
/gene="dJ196E23.1"</pre>
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13615. .13907
  /note="AluSx
                                          /note="MIR2 repeat: matches 97. .138 of consensus"
                                                                                                                                                            22819
                                                                                                                                                                             /note="FLAM_C repeat: matches 131. .2 of consensus"
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/db_xref="GI:2808418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/protein_id="CAB10728.1"
/db_xref="PID:e1240251"
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/protein_id="CAB10729.1"
/db_xref="PID:e1240252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 46. .229 of consensus"
complement(join(17707. .18063,23693. .23746,25506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14838
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/note="AluY repeat: matches 301.
13930. .14980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1 repeat: matches 1194.
12182. .13610
                                                                                                                                                                                                                       'note="MIR2 repeat: matches 146.
                                                                                                                                                                                                                                                                       note="MIR repeat: matches 57. .153 of consensus"
                                                                                                                                                                                                                                                                                                                    note="AluSp repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                            note="MIR2 repeat: matches 14. .103 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                          RGSASTSLPNETLSELETPGKYSLTPPNHWGHPHRYLQHL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:Q99990"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="dJ196E23.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38280. .38493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:Q99991"
/translation="MFSSSFLDKKLYVSRGSASTSLPNETLSELETPGKYSLTPPNHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1MA2_repeat: matches 1.
                                                                                                                                  note="MIR repeat: matches 231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="isoform 1; match: protein 099990"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="GI:2808419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="PID:g2808419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="dJ196E23.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1 repeat: matches 4330. .5384 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="isoform 2; match: protein Q99991"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="isoform 2; match: ESTs R95000 N49626"
                                                                                                               .23433
                                                                                                                                                                                                                                                                                                                                              .21206
                          .26515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .17712
                                                                                                                                                                                                                                                                                               21845
                                                                                                                                                                                                         22714
                                                                                                                                                          23010
repeat:
  matches
                                                                                       conserved"
                                                                                                                                  .47 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1055 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4324 of consensus"
  . 302
                                                                                                                                                                                                                          .21 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2001 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1 of consensus"
of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 25925,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R73306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 25925
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SOURCE
ORGANISM
                                                                                                                KEYWORDS
                                                                                                                                                                                                                                    DEFINITION
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                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49966 TTTTTTTTTTTTTTTTGAGACGGAGTTTCGCTCTTTTTGCCCAGGCTGGAGTGCAATGGC 50025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50026 GCGATCTGGGCTCACCGCAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCC 50085
                                                                                                                                                                                                                                                                                                                                                                                                   50266 G 50266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                    2142 g 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCCCGCCTTGGCTTCCCAAAGTGCTGGGATTACAGGAGTGAGCCAACTGCGCCCCAGCCCA 50265
                                                                                                                                                                                                                                                                                                                                                                                                                                             cacccaccttggcctcccaaagtgttgggattacaggtgtgagccactgcgcctggccaa 2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tagagatggggtttctcccccgttggtcaggctggtcttgaactcccggccttagatgatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGAGACGGGGTTTCTCCACGTTGGTCAGGCTGGTCTCGAACTCCCAACCTCAGGCGATC 50205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttttttttttttttttggacagagttttgctcttgttacccaggctggagtgcaatggc 2383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcctgagtagccaggnttacagccatgcgctaccacgcccggctaatttngtatttnag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCGAGTAGCTGGGATTACAGGCATGCGCCACCACCACGCTAATTTTGTATTTTTAG 50145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcgntctgggctcaccgcaacctctgcctccccagttcaagnaattnttctgcctcggcc 2323
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170820)
                                                                                                                                                                                                                                 Homo sapiens, clone
                                                                       Homo sapiens
                                                                                                                   HTG;
                                                                                                                                                               g4544485
                                                                                                                                                                                                                                                            AC006286
                                                                                                                                         AC006286.9 GI:4544485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%;
Similarity 87.4%;
                                                                                                                   HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 240. .30 of consensus"
33756. .33895
/note="MIR2 repeat: matches 145. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 70. .261 of consensus" 31732. .31863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluJo repeat: matches 295. .1 of consensus" 31461. .31645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1HS repeat: matches 247. 30155. .30352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: 30034. .30352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 145.
29028. .29139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1ME3A repeat: matches 904. .672 of consensus"
33492. .33680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1PA3 repeat: matches 359. .571 of consensus" 30741. .31016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 13. .120 of consensus" 29374. .29473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 18. .154 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MIR repeat: matches 261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR2 repeat: matches 31. .143 of consensus"
                                                                                                                                                                                                                                                       170820 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .30022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29920
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                                                                                                                                                                                                                                    hRPK.21_A_1, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 231; DB 29; Length 123004; Pred. No. 3.30e-153; 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 135. .9 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .84 of consensus"
                                                                                                                                                                                                                                    DRAFT SEQUENCE, 2 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .259 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .571 of consensus"
                                                                                                                                                                                                                                                            30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2203
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JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 Db 148912 CTAAAAATACAAAAATTACCTGGGCTTGGTGGCACATGCCTGTAATCCCAGCTACTCAGGA 148971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 148852 GATCACTTGAGACTGGGAGTTCAAGACCAGCCTGACTAACATGGAGAAGCCCCATCTCTA 148911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                 148972 GGCTGAGGCAGGAGAATCGCTTGAACCTGGGAAGCAGAGGTTGCGGTGAGCCGAGATCGC 149031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2203 gatcatctaaggccgggagttcaaggaccagcctgaccaacgtggagaaaaccccatctcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Ferreira, P., Fitzhlugh, W., Forrest, C., Funke, R.,
Donelan, L., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A.,
Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A.,
Gage, D., Galagan, J., Howland, J.C., Jones, C., Kann, L., Karatas, A.,
Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A.,
McKernan, K., Meddrim, J., Molla, M., Morris, W., Morrow, J.,
Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P.,
Pavlin, B., Peterson, K., Pollara, V., Riey, R., Roberts, D., Roy, A.,
Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C.,
Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H.,
Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                      ggccgaggcagaanaattncttgaactggggaggcagaggttgcggtgagcccagancgc 2382
                                                                                                                                                                                                                                                                                                                                                                                ctnaaaatacnaaattagccgggcgtggtagcgcatggctgtaancctggctactcagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor. This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved
* the accession number will be preserved
* gap of unknown length
* 96190 170820: contig of 74631 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone hRPK.21_A_1
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-JAN-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAR 30, 1999 this sequence version replaced 91:4454493. All repeats were identified using RepeatMasker: Smit, A.F.A. &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
* NOTE: This is a 'working draft' sequence.
   AF134726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Green,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%;
Similarity 87.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         It currently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hRRK.21_A.1"
/clone_lib="RPCI-11 human B:
a 36911 c 37027 g 46132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .170820
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180283 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 232; DB 20
Pred. No. 5.14e-1
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repeat_region repeat_region	, 41 14 170	repeat_region	variation	repeat_region	variation	repeat_region	repeat_region	repeat_region		tariation	repeat region	misc_feature			FEATURES Source		COMMENT S		JOURNAL UI REFERENCE 2	TITLE S	AUTHORS R	134		INITION
0 > > N	/note=	<pre>sgion complement(14461746) /rpt_type=dispersed /rpt_family="AluSx" .</pre>	14451446 /note="cosmid S22 /replace="ctt"	gion c				<pre>sgion complement(420480) /rpt_type=dispersed /rpt_familv="11PA16"</pre>	/note="cosmid S2 /replace="ttct"	/rpt_		- 1	/clone_lib="RPCII1" /chromosome="6"	/db_xref="taxon:9606" /clone="BAC 215012" /map="6p21 3"	Location/Qualifiers 1. 180283 /organism="Homo sapiens"	trum urtp://rtp.genume.wasnington.edu/xw/xepeatmasker.ntml). This sequence overlaps cosmid 822A (AF019413) by 2363 bases and BAC 210G24 (AF129756) by 12177 bases.	Sequencing methodology: high redundancy shotty in plasmids. Sequencing methodology: high redundancy shotty in plasmids. Interspersed Repeats were identified with RepeatMasker (available	Direct Submission Submitted (15-MAR-1999) Department of Molecular Biotechnology, Box	Unpublished 2 (bases 1 to 180283) Rowen.I.	Sequence of the human major histocompatibility complex class III		human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.	1529886 134726.1 GI:4529886	Homo sapiens BAC clone 215012 NG35, NG36, G9A, NG22, G9, HSP70-2, HSP70-1, HSP70-HOM, snRNP, G7A, NG37, NG23, and MutSH5 genes, complete cds. AF134726
	repeat_region		repeat_region		repeat region	1	י פ <i>ו</i> פמר (דפאַדרוו		repeat_region	repeat_region	repeat_region	- 1	repeat region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	- 1	1	repeat_region	repeat_region
<pre>/rpt_type=dispersed /rpt_family="FLAM_C" 84518730 /rpt_type=dispersed</pre>	<pre>/rpt_type=dispersed /rpt_family="L1MB6" 82908425</pre>	<pre>/rpt_type=dispersed /rpt_family="Alusg" 81518263</pre>	<pre>/rpt_type=dispersed /rpt_family="L1MB8" 78528150</pre>	<pre>/rpt_type=dispersed /rpt_family="AluJb" 76897851</pre>	<pre>/rpt_type=dispersed /rpt_family="Alusx" 7486 7688</pre>	01 01	<pre>/rpt_type=dispersed /rpt_family="MER5A"</pre>	<pre>/rpt_type=dispersed /rpt_family="Alusx" 6403</pre>	<pre>/rpt_type=dispersed /rpt_family="FLAM_C" 60996389</pre>	/ + Pt_ Ty Pt Tany Pt Sen /rpt_family="MERSA" 5955.6090	58855938	/rpt_type=dispersed /rpt family="I]ME3A"	/rpt_family="LINE2" 57865873	<pre>/rpt_family="Alusx" complement(56075738)</pre>	<pre>/rpt_family="AluJb" complement(51675468) /rpt_type=dispersed</pre>	<pre>/rpt_tamily="MLT2E" complement(4980, .5112) /rpt_type=dispersed</pre>	complement(49394968) /rpt_type=dispersed		/ipt_raminiy="Alusg" complement(44174729) /rpt_type=dispersed /rpt_fimilu="alusg"	/rpt_type=dispersed	38134084 /rpt_type=dispersed /rpt_family="Alusg"	<pre>/rpt_family="AluSg" complement(37193790) /rpt_type=dispersed /rpt_family="MLT2FA"</pre>	<pre>/rpt_family="Aluy" complement(34163712) /rpt type=dispersed</pre>	<pre>/rpt_type=dispersed /rpt_family="LINE2" complement(30913392) /rpt_type=dispersed</pre>

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                                                                                                                                                                                  85384 TTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAATGGC 85443
85564 TAGAGATGGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCAGACCTCAGGTGATC 85623
                                                                                                                                  85444 GCGATCTCGGCTCACAGCAACCTCCGCCTCCCAGGTTCAAGCCATTCTCCTGCCTCAGCC 85503
                                                85504 TCCAGGGTAGCTGGGATTACAGGCATGCGCCACCACCCGGCTAATTTTTGTATTTTTAG 85563
                                                                                                                                                              2442 tttttttttttttttggacagagttttgctcttgttacccaggctggagtgcaatggc 2383
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Local Similarity 87.4%;
hes 263; Conservative
                                                                                                /rpt_family="Alusx"
complement(9662. .9735)
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8737. .8839
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/rpt_family="AluJb"
complement(10871. .11176)
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/rpt_type-dispersed
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complement(13907. .13
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complement(10427. .10711)
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complement(14378. .14
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/rpt_family-"Alusq"
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/rpt_family="FLAM_C"
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/rpt_family="Alusq"
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_family="FLAM_C"
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_family="TIGGER1"
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                                                                                                                                                                                                                                                    Score 231; DB 31;
Pred. No. 3.30e-153;
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KEYWORDS
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TITLE
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Submitted (08-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 30, 1998 this sequence version replaced gi:3646106. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence is the entire insert of clone 625H18. The true right end of clone 498124 (AL0301657) is at 51918 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS625H18 185371 bp DNA PRI 11-DEC-1998 Human DNA sequence from clone 625H18 on chromosome 6p22.2-23. Contains the gene for ID4 Helix-loop-helix DNA binding protein an part of an alternatively spliced novel gene. Contains ESTS, STSS, GSSS and putative CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 625H18 is from the library RPCI4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
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                                                         island; Helix-loop-helix; ID4
                                                                                                                                                                                                                                                                                                 259.
2889. .2891
/note="clone 498124; cat in this entry; substitution"
/replace="cgt"
                                                                                                                                                                                                                                  /note="clone 498124; ggc in this entry; substitution"
/replace="gtc"
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/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                    /map="p22.2-23"
                                                                                                                                                                                                                                                                                                                                                                                      /clone="625H18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/replace="tct"
4651. 4653
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/note="Tigger3(Golem) repeat: matches 1. .9
3177. .3243
/note="MLT1A2 repeat: matches 284. .351 of
3673. .3675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="close 498124; caa in this entry; substitution" /replace="gga" 3774. .3776
                                                                                                                                                                            /replace="cgt"
6774. .6776
                                                                                                                                                                                                                                                                                                                                                                                                               /note="clone 498I24;
/replace="cgt"
5701. .5703
/note="clone 498124; ttc in this entry; substitution" /replace="tcc" 7288. .7291
                                                                                                                                                                                                                                                                                               complement(6131. .6656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5444. .5447
                                                                                                                                                                                                                                                                                                          /note="clone 498I24; acg in this entry;
/replace="atg"
                                                                                                                                                                                                                                                                                                                                                                                  /note="clone 498I24;
/replace="gta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="clone 498124;
/replace="cgt"
4865. .4867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="clone 498I24; ata in this entry; substitution"
/replace="aca"
                                                                                                                                               /note="clone 498I24;
/replace="gct"
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/replace="tct"
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/replace="atcg"
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/replace="cgg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="L1MD2 repeat:
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/replace="cat"
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/replace="gca"
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/replace="cgg"
                                                        note="clone 498124;
replace="aga"
                                                                                                   /note="clone 498124;
/replace="tac"
                                                                                                                                                                                                       note="clone 498124;
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                                                                                                                                                                                                                                                                              note="match: GSSs AQ224537 B56744"
                                                                                                                                                                                                                                                                                                                                         note="AluSq repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace="agt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "L2 repeat: matches 2559. .2733 of consensus"
   .4047
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                                                                         <u>a</u>aa
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Note: remainder of annotations omitted
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/note="clone 498124; (

/replace="gcg"

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/note="clone 498124; a

/replace="aaa"

10765...10939
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/note="clone 498124; (
/replace="aa"
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/note="clone 498124;
/replace="gtc"
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/note="clone 498I24;
/replace="cgt"
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/replace="cagaga"
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/note="clone 498I24;
/replace="gcc"
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/replace="agt"
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/replace="tcgg"
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10485. .10764
                                                                                                                                                                                                                                                                                                                                                                                             /replace="cat"
10219. .10220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER6 repeat: matches 1. .697 of consensus" 10038 . 10040 / 10038 . 10040 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 10048 / 1004
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/replace="ttg"
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/replace="ctt"
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'note="clone 498I24;
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'replace="gcc"
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/note="clone 498124;
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/note="clone 498124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )517. .9519
'note="clone 498I24;
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                                                       'note="MER6 repeat:
                                                                                                                                                                                                                                                                         .0485. .10764
note="Alux repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluY repeat: matches 1. .304 of consensus"
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                                                                                                                                                                                                                                                                                 matches 1. .285 of consensus*
                                                          matches
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                                                                                                                                        substitution"
                                                       consensus"
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Query Match 9.5%; Best Local Similarity 87.4%; Matches 264; Conservative

Score 232; DB 29; Pred. No. 5.14e-154; 0; Mismatches 38;

Length 185371;

Indels

0;

Gaps

0;

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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-JUN-1996) E-mail enquiries: humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk important: This sequence is the entire insert of clone B10B1. The true left end of clone B10B1 is at 1 in this sequence. The true right end of clone B10B1 is at 40926.

B10B1 is from the human chromosome 22-specific cosmid library (SC22CB) constructed at the Sanger Centre by Mark Ross and Cordelia Langford. This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre
                                                                                                                                                                                                                                                                                                                       chromosome 22 mapping group.
Further information can be found at http://www.sanger.ac.uk/HGP/Chr22/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSB10B1 40926 bp DNA PRI Human DNA sequence from cosmid B10B1 on chromosome ESTs, CA repeat and STS, complete sequence.
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Primates; Catarrhini; Hominidae; Homo.
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   /note="25 copies of AC 100 % conserved; Polymorphic by comparison with Z17028"
                                                                                    5618. .5672 /note="MIR element fragment" 8057. .8385
                                                                                                                      /note="match: EST T07591 clone HFBEL36" 5618. .5672
                                                                                                                                                        /note="MIR element fragment"
2517. .2795
                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                               /note="match: Z17028 DNA segment containing (CA) repeat"
                                                                                                                                                                                                                         /clone="B10B1"
                                                                                                                                                                                                                                                             /chromosome="22"
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Similarity 86.6%;
264; Conservative
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/note="Alu repeat:
9179 c 9923 g
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16538 AAGTTGAGGCCGAGGCGCAGGGCTCACGCCTGTAATCTCAGCACTTTGGGAGGCCGAGGC 16597
                                                                                                                                                                                                           16598 AGGCGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAACATGGAGAAACCCCAT 16657
                                         16718 CGGGAGGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAATGAGCCGAG 16777
caggaggccgaggcagaanaattncttgaactggggaggcagaggttgcggtgagcccag
                                                                                                     CTCTACTAAAAATACAAAATTAGCCGGGCGTGGTGGCGCATGCCTGTAATCCCCAGCTACT 16717
                                                                                ctctactnaaaatacnaaattagccgggcgtggtagcgcatggctgtaancctggctact
                                                                                                                                                                999t99atcatctaaggccgggagttcaagaccagcctgaccaacgtggagaaaccccat
                                                                                                                                                                                                                                                    aagtettggccaggcgcagtggctcacacctgtaatccccaacactttgggaggccaaggt 2197
                                                                                                                                                                                       /note-"Could be 5 G's" 39390. 39700
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/note="match:STS G03723"
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/note="MIR element fragment"
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9674. 9749
/note-"MER33 element fragment"
11611. .11752
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30874. .30968
/note="MIR2 element fragment"
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'note="11 copies of 3 mer 88 % conserved"
18668. .18958
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1762. .11898
                                                                                                                                                                                                                                                                                                                                                            Score 229; DB 29;
Pred. No. 1.36e-151;
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11143 t
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Best Local Similarity 86.9%;
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                         68860
                                                                                                                                                                                    68740 TCCTGAGTAGCTGGGATTACAGGCATGTGCCACGCCCGGCTAATTTTTGTATTTTGTAG 68799
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                                                                                                                                                                                                                                                                                                         2442 tttttttttttttttggacagagttttgctcttgttacccaggctggagtgcaatggc 2383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCC 68917
                                                                                                  TAGAGACGGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGATC 68859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaaaa 2442
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                                                            tagagatggggtttctccacgttggtcaggctggtcttgaactcccggccttagatgatc 2203
                                                                                                                                           tcctgagtagccaggnttacagccatgcgctaccacgcccggctaatttngtattttnag 2263
MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens clone DJ0649M07, WORKING DRAFT SEQUENCE, 2 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC006968.1 GI:4337292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 96115)
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/clone="DJ0649M07"
18141 c 17098 g 28024 t
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7 21694: gap of unknown length
5 96115: contig of 74421 bp in length
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                  Score 226; DB 20;
Pred. No. 3.60e-149;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 96115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
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FEATURES
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           only a small overlap. This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre chromosome 22 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22/
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone requests: clonerequest@sanger.ac.uk
on May 28, 1998 this sequence version replaced gi:1772948.
IMPORTANT: This sequence is the entire insert of clone 302D9.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The true right end of clone 302D9 is at 145871. 302D9 is from the library RPCII constructed at the Roswell Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The true left end of clone 302D9 is at 1 in this sequence. The true right end of clone 415G2 is at 55164.

The true left end of clone 282F2 is at 69679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DNA sequence from PAC 3021
Contains STS, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                       889.
                        /note="AluY repeat: matches 2. .301 of consensus"
3747. .3922
/note="MLTIE repeat: matches 188. .365 of consens
                                                                                                                                                                                                                                         /note="MIR repeat: matches 20. .160 of consensus" 2359. .2659
                                                                                                                                                                                                                                                                                                    1446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSx repeat: matches 1. .302 of consensus" 585. .759
                                                                                                                                                                                                                                                                                                                                                         /note="MER5A repeat: matches 71. 1029. .1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188.
                                                                                                                                                                                                                                                                                                                          /note="AluSp repeat: matches 303. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER3 repeat: matches 209. .155 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="q11.2-qter"
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/db_xref="taxon:9606"
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                                                                                                                                               'note="AluSq repeat:
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                                                                                                                                                                                                       'note="AluSc repeat: matches 299.
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                                                                                                                                                  matches 302.
                               .365 of consensus
                                                                                                                                                                                                          .3 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                        .26 of consensus"
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/note="MLT1E repeat: matches 382.
5188. .5488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7479. .7751
/note="AluJo repeat: matches 9.
7773. .8057
                                                       /note="ITG in clone 415G2"
/replace="ttg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="THE1B repeat: matches 3. .364 of consensus" 4296. .4482
                                                                                                                                                                                                            /note="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="CTG in clone 415G2"
/replace="ctg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR2 repeat: matches 146.
8911. .9027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7773. .8057
/note="AluJo repeat: matches 2.
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/note="AluSg repeat: matches 299. .1 of consensus"
6386. .6447
/note="MIR2 repeat: matches 141. .59 of consensus"
                                                                                                                                                                                                                                                             'note="MLT1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="MIR repeat: matches 262.
3107. .9277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7036
note="MADE1 repeat: matches 33.
                                'note="AluY repeat: matches 300.
                                                                                                                                                                                                                                                                                                                                                                                                           "e="MIR repeat: matches 91. .189 of consensus"
17. .14057
                                                                                                                                                                                                                                                                               e="MIR repeat: matches 49. ,233 of consensus"
)1. ,15396
                                                                                                                                                                                                                                                                                                                                                                                                                                           e="MIR repeat: matches 191. .76 of consensus"
24. .13916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="MSTA repeat: matches
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Le="FAM repeat: matches 161.
7. .10222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="MIR repeat: matches 91. .262 of consensus"
                                                                                                                                e="AluSc repeat: matches 1.
1. .16243
                                                                                                                                                                             e="MLT1B repeat: matches
                                                                                                                                                                                                                                                                                                              e="MIR repeat: matches 137. .225 of consensus" 5. .15037
                                                                                                                                                                                                                                                                                                                                          e="AluSg repeat: matches 300. .1 of consensus"
7. .14449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="AluSp_repeat: matches 302. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e="CGT in clone 415G2"
lace="cqt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="MIR repeat: matches
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                                                                                                                                                                                                                                                                                                                                                                            e="MIR repeat: matches 29. .146 of consensus"
8. .14364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lace="cg1
                                                                                                             e="MLT1B repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e-"MIR repeat: matches 20. .137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="MIR repeat: matches 150.
5. .11943
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 repeat: matches 1.
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                                                                                                                                                                               119.
                                                                                                                 188.
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82
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                                 .2 of consensus"
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Matches 25
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               13458 ATGATCTCAGCTCACACACCTCTGCCTCCCAGGTTCAAGCAATTCTTCTGCCTCAGCC 13517
                                                         2442 ttttttttttttttttggacagagttttgctcttgttacccaggctggagtgcaatggc 2383
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2382 gcgntctgggctcaccgcaacctctgcctccccagttcaagnaattnttctgcctcggcc 2323
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                                                                                                                     Match 9.3%;
Local Similarity 86.9%;
les 259; Conservative
                                                                                                                                                                                annotations omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJo repeat: matches incomplete repeat" 25457. 25%/0
                                                                                                                                                                                                                            /replace="26801..26
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/note="AGT in clone 415G2"
/replace="agt"
                                                                                                                                                                                                                                                                        /replace="tca"
26733. .26734
                                                                                                                                                                                                                                                                                                                                                                                                                                          25638. .25934
                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSq repeat: matches
25974. .26236
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/note="TAAAAG in clone 415G2"
/replace="taaaag"
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/replace="ttg"
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                                                                                                                                                                                                            'note="MIR repeat: matches 92. .218
                                                                                                                                                                                                                                                        26733. .26734
'note="GAC in clone
                                                                                                                                                                                                                                                                                                    16699. .26701
'note="TCA in clone 415G2"
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replace="cag"
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'replace="cgt"
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replace="tta"
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                                                                                                                                                                                                                                                                                                                                                                         ncomplete repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MIR2 repeat: matches 143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace="tga"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace="act"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="Alusq repeat: matches 303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te="AluSx repeat: matches 1. .302 of consensus"
57. .24723
te="match: STS L17928"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2. .25544
e="TCA in clone 415G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    lace="tca"
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21967
                                                                                                                     Score 226; DB 29;
Pred. No. 3.60e-149;
0; Mismatches 39;
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                                                   29658 AATTCTTGGCCGGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAAGCCAAGGT 29717
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2138 aagtottggccaggcgcagtggctcacacctgtaatcccaacactttgggaggccaaggt 2197
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                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cambridgeshire, CBIO ISA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: Clonerequestssanger.ac.uk
On Mar 23, 1999 this sequence version replaced gi:4468894.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJ500L14 Contig_ID: 00165
acc=AL023583 Length: 10585 bp Unfinished: dJ500L14 Contig_ID: 01706 acc=AL023583
Length: 10585 bp Unfinished: dJ500L14 Contig_ID: 01706 acc=AL023583
Length: 10595 bp Unfinished: dJ500L14
Contig_ID: 01917 acc=AL023583 Length: 1050 bp Unfinished:
dJ500L14 Contig_ID: 01722 acc=AL023583 Length: 1850 bp
Unfinished: dJ500L14 Contig_ID: 02443 acc=AL023583 Length:
dJ500L14 Contig_ID: 02540 acc=AL023583 Length:
1014 bp Unfinished: dJ500L14 Contig_ID: 01799 acc=AL023583
Length: 1244 bp Unfinished: dJ500L14 Contig_ID: 01123
acc=AL023583 Length: 59868 bp Unfinished: dJ500L14
Contig_ID: 03010 acc=AL023583 Length: 18171 bp Unfinished:
dJ500L14 contig_ID: 03010 acc=AL023583 Length: 18171 bp Unfinished:
* MOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as conn as 't 'is available and the accession number will
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                                                                                                          262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160258)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mashreghi-Mohammadi,M.
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                                                                                                                                   Similarity
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                                                                                                          Conservative
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                     /clone="500L14"
33126 c 3277
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                                                                                                     Score 226; DB 19;
Pred. No. 3.60e-149;
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29718 GGGCAGATCATCTGAGGCTGGGAGTTCAAGACCAGCCTGACCAACATGGAGAAACCCCGT 2977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29838 TGGGAGGCTAAGGCAGAGAATTGCTTGAACCCAGGAGGCGGAGGTTGTGGTGAGCCGAG
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Human DNA sequence from clone 821D11 on chromosome 22q12.3-13.1.
Contains three partial unknown genes, one downstream of a predicted CpG island, and the first coding exon of the SREBF2 gene for Sterol Regulatory Element Binding Transcription Factor 2 downstream of a predicted CpG island. Contains ESTs, STSs, GSSs and genomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is not the entire insert of clone 821D11. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone 250D10 (299716) is at 76628 in this sequence. The true right end of clone 10966 (AL023879) is at 42082. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-AUG-1998) E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 12, 1998 this sequence version replaced gi:3355590. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                    This sequence was generated from part of bacterial clone contigs human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22 B2DDI is from the library RPCI5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 76727)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                feature key
∕organism="Homo sapiens"
                                                                                   Location/Qualifiers
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                /note="AluY repeat: 5359. .5361
                                                                                                                                                                                                                                                                                                                           /note="AluSp repeat: matches 297. .2 of consensus" complement(3457. .3551) /note="MLR repeat: matches 149. .59 of consensus" complement(3552. .3847)
                                                                                                                                                    /replace-"ttttatttat
complement(4800. .50
                                                                                                                                                                                                                                                                                                                                                                                               /note="LIMC1 repeat: matches 1079.
complement(3162. .3456)
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1314. .1316
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complement(445. .743)
                                                 complement (5128.
                                                                 /note="clone 109G6; ttttat in
/replace="tt"
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/note="clone 109G6;
                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3042. .3133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="clone 109G6; gga in
/replace="gaa"
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1773. .1895
                                                                                                                                                                                                                                       note="clone 109G6; tt in this replace="ttgagt"
                                                                                                                                                                                                                                                                         'gene="dJ821D11.1"
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/replace="tta"
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/product="dJ821D11.1 (PUTATIVE protein)"
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/clone="821D11"
                                                                                                   gene="dJ821D11.1"
                                                                                                                                                                                                                                                                                                           'note="AluJb repeat: matches 299.
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/db_xref="GI:4200330"
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/product="dJ821D11.1 (PUT!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="this gene and dJ821D11.2 could be
natch: ESTs AA419437 AA332515"
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                                                                                                                                   note="AluSq repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MIR repeat: matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MLALTLAKADSPRTALLCSAWLLTASFSAQQHKGSLQKDPLLSQ
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                                 matches 300.
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/gene="dJ821D11.1"
/note="clone 109G6;
/replace="ctg"
10969. .10971
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/replace="att"
5772. 5773
                                                                                                                                                                                                                                                                                                    9047. .9049
/gene="dJ821D11.1"
/note="clone_10966; gcg in this entry; substitution"
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complement(10457...10754)
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complement(9948. .10250)
                                                                                                                                                                                                                                         /note="AluJo repeat: matches 123.
complement(9330..9609)
                                                                                                                                                                                                                                                                             complement (9207.
                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8708. .8887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Alusx repeat: matches 302.
complement(8307...8606)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7895.
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/note="23 copies 2 mer tt 87%
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/note="AluSq repeat: matches 300.
                                                                                                                                                                                                                                                                                                                                                       3898. .9197
/note="AluSx repeat: matches
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                                                                               replace-"cac"
                                                                                                  /note="clone 109G6;
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/note="MIR2 repeat: matches 79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="clone 109G6; att in this entry; substitution"
/replace="act"
                                                                                                                                                     'note="AluSg repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER46 repeat: matches 88. .232 of consensus"
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                                                                                                                    'gene-"dJ821D11.1"
                                                                                                                                                                                                                                                                                                                                                                                                  'note="AluJb repeat:
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'replace="ctg"
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replace="cag"
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/replace="ttt"
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BASE COUNT
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Best Local Similarity 87.8%;
Matches 252; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57514 TGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAAACCCCCGTCTCTACTAAAAATACAAA 57573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57574 ATTAGCCGGGCGTCGTGGCACATGCCTGTAATCCCAGCTACTCAGGAGGCTAAGGCAGGA 57633
                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2216 cgggagttcaagaccagcctgaccaacgtggagaaaccccatctctactnaaaatacnaa 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL Submitted (16-MAR-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
On Mar 21, 1999 this sequence version replaced gi:4375971.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJ469D22 Contig_ID: 01101 acc=AL031284
Length: 61683 bp Unfinished: dJ469D22 Contig_ID: 01792
acc=AL031284 Length: 22802 bp.
* * NOTE: This is a 'working draft' sequence.
* * This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS469D22 85285 bp DNA
Human DNA sequence *** SEQUENCING IN PROGRESS ***
469D22, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 85285)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                 a
                                                                                                                              /organism="Homo sapiens"
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/note="clone 109G6; ggc in this entry; insertion"
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Pred. No. 9.48e-147;
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from clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently * consists of 17 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC005087 105984 bp DNA HTG 12-JUN-1998
Homo sapiens clone RG306D19, WORKING DRAFT SEQUENCE, 17 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19080 TGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCTGGCCCA 19139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2322 tcctgagtagccaggnttacagccatgcgctaccacgcccggctaatttngtatttnag 2263
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Chacko,J., Chen,J., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Ganesh,R., Garcia,C., Goodman,M., Gorrell,J.H., Haywood,M., Hernandez,J., Jackson,L., Jin,S., Kampal,R., Karpathy,S., Kovar,C., Lau,S., Leal,B., Lee,E., Li,Y., Lichtarge,O., Liu,W., Logan,O., Liu,J., Ly,T., Marondel,I., Martinez,C., Merscher,S., Montgomery,K., Oswal,G., Perez,L., Rashid,N.D., Renault,B., Rowland,K., Savage,L., Scherer,S.E., Shen,H., Simon,M., Stovall,K., Timms,K.M., Todd,J., Vo,Q., Williamson,A., Worley,K.C., Yu,W., Kucherlapati,R.,
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l Similarity 83.6%;
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Muzny,D., Arenson,A.D., Adams,C., Bunac,C.,
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/db_xref="taxon:9606"
/clone="RG306D19"
22089 c 23772 g 29000
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37078: contig of 6123 bp in length
37095: gap of unknown length
45603: contig of 8508 bp in length
45620: gap of unknown length
53337: contig of 7717 bp in length
60507: contig of 7717 bp in length
60524: gap of unknown length
60524: gap of unknown length
69631: contig of 9107 bp in length
69648: gap of unknown length
69648: contig of 15630 bp in length
85278: contig of 15630 bp in length
85295: gap of unknown length
85296: contig of 15630 bp in length
85298: contig of 16630 bp in length
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Pred. No. 9.48e-147;
0; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-JUN-1998) Human Genome Seq
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 114842)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-MAY-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-OCT-1997) Molecular and Human Genetics, College of Medicine, One Baylor Plaza, Houston, TX 770 3 (bases 1 to 114842)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.
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Direct Submission
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Direct Submission
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Direct Submission
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                                               /rpt_family="Alusg/x"
2130. .2429
                                                                                                                                                                                                 /rpt_family="MIR"
1665. .1803
                                                                                                                                                                                                                                                                                                     /note="Overlaps bases 1-226 in AC003029."
/note="Region: Overlaps with AC003029."
complement(join(26. 139,883. 1011.1511. 1622,6099. .6178,8147. 8287,9423. .9527,24349. .24498)]
/note="X05409|HSALDHII Human RNA for mitochondrial aldehydrogenase I ALDH I (EC 12.1.3). This clone contains only the first 7 exons of the gene."
/gene="Human mitochondrial aldehyde dehydrogenase I"
complement(381. .672)
                                                                                                                                                                                                                                                        /rpt_family="AluJo" complement(1255. .14
       /rpt_family="Alusg" 2169. .2419
                                                                                                                                                          /rpt_family="MER4C" 1811. .1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="12q24"
                                                                                                                                /rpt_family-"MER5A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="12"
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/db_xref="taxon:9606"
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/rpt_family="MER20"
complement(3215...3385)
/rpt_family="AluSq"
complement(3389...3695)
/rpt_family="AluSq"
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complement(5704. .6003)
/rpt_family="AluSx"
6551. .6829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AluSg"
complement(8874..9007)
/rpt_family=""""
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| 14967. .15038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10319. .10604)
/rpt_family="AluJo"
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complement(9779. .10261)
/rpt_family="MLT1G"
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complement(8542. .88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluSg"
complement(7122. .73
/rpt_family="AluJo"
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/rpt_family="AluSq"
complement(4220..4522)
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                                                                                                                                                          complement(17582. .17681)
/rpt_family="L2"
17852. .17996
                                                                                                                                                                                                                                              /rpt_family="AluSx" complement(14834...
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complement(14166. .14334)
/rpt_family="MIR"
14462. .14746
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11956.
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/rpt_family="L2"
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            /rpt_family="FRAM"
18785. .19082
                                                                    /rpt_family="Alusp"
complement(18483. .
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12290. .12580
/rpt_family="AluJb"
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complement/ser/
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complement/incom
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                                                                                                               /rpt_family="Alu"
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rpt_family="Alusg"
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. _4897
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3. .13270
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                                         _family="AluSc"
6. .18770
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RESULT LOCUS

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HS230G1

125515 bp

VA PRI 05-AUG-1998 from PAC 230Gl on chromosome Xpll.3

DEFINITION
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KEYWORDS

g3319673 Z84466.1 GI:3319673 HTG; Xp11.3.

Homo sapiens DNA sequence from PAC 230Gl on c Contains EST, STS and GSS, complete sequence. Z84466

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Best Local Similarity 84.9%;
Matches 265; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99162 AAAAATTGTAAATCTGGGCCAGGTGTGGTGGTCGCTCACTCCTGTAATCCCACCACTATGGGA 99221
                      99462 AAAACAAACAAA 99473
                                                                                                                             99402 TGAGCCAAGATCGTGCCATTGCACTCCAGCCTGGGCAACAAGAGCAAAACTCCATCTCAA 9946
                                                                                                                                                                                                                   99342 CCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAG 9940:
                                                                                                                                                                                                                                                                              99282 AAACCCCACCTCTACTAAAAATACAAAATTAGCCGGGCATGGTGGCGCATGCCTGTAATC 99341
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2429 aaaaaaaaaaa 2440
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                                                                                    tgagcccagancgcgccattgcactccagcctgggtaacaagagcaaaactctgtccaaa 2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="GC_rich"
complement(24564. .24588)
/rpt_family="GC_rich"
24653. .24715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(22010. .22164)
/rpt_family="AluJo/FRAM"
complement(22458. .22743)
/rpt_family="AluJo"
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/rpt_family="AluSx"
complement(20059. .20331)
/rpt_family="AluJo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="MIR" 24417. . . 24457
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/rpt_family="FLAM_C"
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/rpt_family="MIR"
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20803. .20981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluJb"
20516. .20802
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lement(21500
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This sequence was generated from part of bacterial clone contigs of human chromosome x, constructed by the Sanger Centre chromosome x mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX/

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-JUL-1998) Chromosome X Project Group (http://www.sanger.ac.uk/HGP/ChrX/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 15, 1998 this sequence version replaced gi:2578073.
IMPORTANT: This sequence is the entire insert of clone 23021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           During sequence assembly data are compared from overlapping clones Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
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1 (bases 1 to 125515)
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                                                                                                                                                                                                                                     /note="match: STS AL023622" 3775. .4139
                                                                                                         /note="AluJb repeat: matches 297.incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                     /note="L1 repeat: matches 3546.
3477. .3772
                                                      note="Alusg repeat: matches 300.
                                                                                                                                                                                                                                                                                                                                                                                                                                   note="FLAM_C repeat: matches 132. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1 repeat: matches 3812. .3573 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluJo repeat: matches 47. .300 of consensus;
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="X"
/map="p11.3"
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/db_xref="taxon:9606"
   'note="AluJb repeat: matches 135.
                                                                                                                                                                                                                                                                                                                'note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="MIR repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSp repeat: matches 234. .301
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                                                                                                                                                                                                 repeat: matches 2593. .2227 of consensus
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.1 of consensus;
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/note-"match: multiple ESTs; match: H19527 H19455 H12759 AA114161 H20205; match: H12802 AA606420 D55951 F10557 R22909; match: H59758 AA904128 AA332774 T85326; match: AA687697 H48153 H20397 R83683 AA454735; match: AA687697 H44059 H21221 AA321798; match: H46375 H19843 A573937 AA868327 AA865942; match: AA570700 H44150 H20192 T88882 AA015618; match: H20383 T15663 H49938 H59757
                                                                                                                                                                                                                 27043. .27125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1.
10721. .10781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER39 repeat: matches 226.
9423. .9725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1 repeat: matches 1982. .1612 of consensus" 6620. .6923
                                                                                                                                                                                        /note="L1MB8 repeat: matches 922. .840 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    incomplete repeat"
5940. .6297
                                                                                                                                                                                                                                          /note="MADE1
                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 152.
                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Alusx repeat: matches 298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L1PB3 repeat: matches 746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 259. .30 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluJo repeat: matches 301. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1 repeat: matches 4285. .4647 of consensus"
11619. .11917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10407
                                                                                                                                                                                                                                                                                                                                                                               note="FLAM_C repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="MIR repeat: matches 134. .18 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MER31 repeat: matches 3. .328 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note-"AluSq repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluJb repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1 repeat: matches 3705. .3766 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluJb repeat: matches 296. .3 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="AluSp repeat: matches 2. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER21B repeat: matches 14. .541 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluSq repeat: matches 303. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Alusg repeat: matches 297. .11 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MER42c repeat: matches 283. .187 of
                                                                                                                                                                                                                                                                                                                 .24575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .22400
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                                                                                                                                                                                                                                                                                                                                                                .24071
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                                                                                                                                                                     .>32667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 145. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 301. .1 of consensus"
                                                                                                                                                                                                                                       repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 298. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                       matches 262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 297. .1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      matches 302. .1 of consensus"
                                                                                                                                                                                                                                       .80 of consensus
                                                                                                                                                                                                                                                                                      .102 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .23 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .301 of consensus
                                                                                                                                                                                                                                                                                                                                     .90 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .297 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .97 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .883 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .380 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consensus"
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Note: remainder of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70117 TGGCCAGGCGTGGTGGCTCATGCCTGTAATCCTAGCACTTTGGGAGGCCAAAGCGGGTGG 70176
                                                                                                                                                                              70297
                                                                                                                                                                                                                                                                                                                                                                                                                   70177
                                                                                                                                                                                                                                                                                               70237
      2384
                                                                                                                                                                                                                                        2264
                                                                                                                                                                                                                                                                                                                                                         2204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 8. .167 of consensus" prim_transcript <37193. .>42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 9.2%;
Local Similarity 86.3%;
hes 258; Conservative
                                                      TAAAAATACAAAATTAGCCAGGTGTGGTGGCACATGCCTGTAATCCCAGCTACTTGGGAG 70296
                                                                                                                                                                                                                                                                                                                                                     atcatctaaggccgggagttcaagaccagcctgaccaacgtggagaaacccccatctctac 2263
                                                                                                                                                                                                                                                                                                                                                                                    ATCACCTGAGGTCGGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCCATCTCTAC 70236
                                                                                                             gccgaggcagaanaattncttgaactggggaggcagaggttgcggtgagcccagancgcg 2383
                                                                                                                                                                          GCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGCG 70356
                                                                                                                                                                                                                                 tnaaaatacnaaattagccgggcgtggtagcgcatggctgtaancctggctactcaggag 2323
/note="match: multiple ESTs; match: AA282955 AA139749
AA571767 AA464040 AA824013; match: Z21451 AA895634 H34312
F23024 W46758 H34604; match: AA718679 W39769 AA592343
AA492206 W54246; match: AA173069 AA425177 AA073466 M85747
AA768214; match: AA529912 AA680646 AA569136 AA896025
AA795810; match: AA523912 AA680646 AA569136 D57292;
match: AA800504 AA275500 N34338 AA416411 AA468169; match: AA8075780 N34338 AA416411 AA468169; match: AA177766 AA634885 AA807799 C886673 N49127; match: AA17503
AA1057768 AA412556 C81242 AA003577; match: AA2790027
AA105708 AA412556 C81242 AA003577; match: AA2730097
AA882016 H86687 C81219 H33662; match: AA4750097
AA882016 H86687 C81219 H33662; match: Z98492 AA233775
T08746 AA433377 AA6619526; match: R69671 AA435188 AA760097
H99588 AA763904"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: multiple ESTs; match: R16511 T19961 R41881 N48906 T19960; match: AA458501 H05270 AA442994; match: AA144152 AA119507 AA851630 AA114188 AA866788; match: AA104043 W88083 AA231365 AA637261 W98335; match: AA434797 AA518513 AA119507 AA800636 AA866788; match: R17266 R96026 AA346254 AA134624 R71984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS G23742 G06335 G22442"
32725. 32762
/note="19 copies of 2 mer 97 % conserved"
<32821. >32877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA182732; match: R16808 AA477697 T85154 H48170 R83682; match: H51394 AA573455" <32049. .32643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER440 repeat: matches 728. .4 of consensus" 41470. .41739 /note="Alusq repeat: matches 303. .35 of consensus; incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: multiple ESTs; match: H16234 H59757 AA182732 AA477696 R23011; match: T85154 AA573937 R83682 AA454787 AA236603; match: H45737 T77405 F13363 N76413 W85093" 35727 ...35875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 188. .68 of consensus" 39826. .40528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44018. .44331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 260. 39291. .39412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR2 repeat: matches 146. .34 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: 3' EST AA033820 clone 375753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .38485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .43642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 223; DB 29; Length 125515; Pred. No. 9.48e-147; 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .84 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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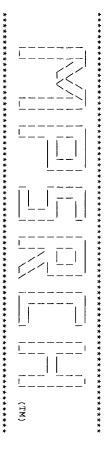
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QΥ B Qy B QΥ Db

δÃ Db. Qy

> Search completed: Tue Jan Job time: 4528 secs. 18 14:34:00

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 18 13:21:10 2000; MasPar time 13.66 Seconds 695.319 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-09-246-129-2 (1-174) from US09246129A.pep 1314 1 MRRFLSKVYSFPMRKLILFL......DISLVDYTKEDKTFFGAFLL 174

Scoring table: PAM 150 Gap 11

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 43.857; Variance 76.268; scale 0.575

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21212233333333333333333333333333333333	Result
225 226 2208 2208 2203 2203 2203 2203 2194 1194 1177 1177 1177 1157 1157 1157 1157 115	Score
115.00 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Query Match 1
240 44 2240 44 2240 44 233 66 233 11 233 11 233 11 233 14 24 24 5 11 31 6 11 3	Length DB
0751217 0743557 0777764 0735853 0735853 0757764 0757764 0757764 0757764 075776	3 ID
LIGAND. LIGAND FOR HERPESVIRUS TUMOR NECROSIS FACTOR TUMOUR NECROSIS FACTOR TNF-ALPHA. TUMOR NECROSIS FACTOR TRANCE (FRAGMENT). TRANCE (FRAGMENT). TOMOR NECROSIS FACTOR TRANCE (FRAGMENT). TOMOR NECROSIS FACTOR TOMOR NECR	Description
1.59e-24 4.26e-22 4.26e-19 2.52e-19 2.52e-19 2.52e-11 2.39e-17 2.04e-15 4.93e-11 9.83e-11 9.83e-11 1.19e-16 1.71e-06 1.71e-06 2.70e-02 7.61e-02 7.61e-02 7.61e-02 7.61e-02 7.61e-02 7.61e-02 7.61e-02	Pred. No.

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016241	P95600	P72284	Q40763	033261	051688	066916	053115	053611	023433	P73387	Q90755	Q94240	P79783	P73139	068614	Q90753	034573	067272	Q63928	064485	Q45757	Q99761	009126	049868
T	\vdash	FIXNC (EC 1.9.3.1).	CELLULASE PRECURSOR.	L-ASPARAGINE PERMEASE.	OLIGOPEPTIDE ABC TRANS	CATION EFFLUX SYSTEM (ISOCITRATE DEHYDROGENA	ISOCITRATE DEHYDROGENA	HYPOTHETICAL PROTEIN.	HYPOTHETICAL 18.0 KD P	BRM PROTEIN.	COSMID F55A4.	CMP-NEUAC:GM3 SIALYLTR	HYPOTHETICAL 418.3 KD	HYPOTHETICAL 34.5 KD P	BRG1 PROTEIN.	YFKT PROTEIN.	ABC TRANSPORTER.	BRAHMA RELATED PROTEIN	F20D22.1 PROTEIN.	DELTA-ENDOTOXIN (FRAGM	LYMPHOTOXIN BETA ISOFO	SEMAPHORIN J (SEMAPHOR	PUTATIVE RIBOPHORIN I
2.83e+00	2.83e+00		2.83e+00	2.83e+00	2.83e+00	2.06e+00	2.06e+00	2.06e+00	2.06e+00	2.06e+00	1.50e+00	1.50e+00	1.50e+00	1.09e+00	1.09e+00	5.67e-01	7.86e-01	5.67e-01	4.08e-01	4.08e-01	4.08e-01	4.08e-01	2.93e-01	2.93e-01

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Eding	RESULT	Qy	Db	Qy	Db	Qy	Db	Que Bes Mai	SQ	DR S	DR R	RL	RA	ద	R R		g	SO	ן כ		Di	å	RESULT
01-NOV-1998 (TREMBLREL. 08, CREATED) 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) LIGAND FOR HERPESVIRUS ENTRY MEDIATOR.	T 2 075476 PRELIMINARY; PRT; 240 AA.	142 SLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL 174	LYVNISQLSLINF-EE	83 SECSEIRQAGRPNKPDSITVVITKVIDSYPEPTQLLMGTK-SVCEVGSNWFQPIYLGAMF 141	QPLNH-KVYM-R-NSKYPGDLVLMEEKRLNYCTTGQIWAHSS	23 PVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMT 82	-IP-LEWEDTYGTALISG-VKYKKGGLVINEAG	Query Match 17.1%; Score 225; DB 11; Length 279; Best Local Similarity 34.6%; Pred. No. 1.59e-24; Matches 53; Conservative 32; Mismatches 51; Indels 17; Gaps 13;	SEQUENCE 279 AA; 31340 MW; 9062DF08 CRC32;	PEAM: PEO0229: TNF: 1.) TO EMBL/GENBANK	FENNER M.H., SHIODA T., ISSELBACHER K.J.;	STRAIN-BALB/C;	[1] SEQUENCE FROM N.A.	UROGNATHI; MURIDA	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;	MUS MUSCULUS (MOUSE).		(TREMBIREL OL, LAST	1996 (TREMBLREL. 01, CREATED)		T 1 061217 PRELIMINARY: PRT: 279 AA.

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RESULT
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AC 04
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Matches 4
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7 PRELIMINARY; PRT; 240 AA.
043557
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLEL. 06, LAST ANOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER LIGHT. HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MANMA
                                                                                                                                                                                                                                                                                                                                                                                                IMMUNITY 8:21-30(1998).
EMBL; AF036581; G2815624; -.
SEQUENCE 240 AA; 26351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WARE C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAÜRI D.N., EBNER R., MONTGOMERY R.I., KOCHEL K.D., (YU G.-L., RUBEN S., MURPHY M., EISENBERG R.J., COHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMOH
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CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
  155
                                                                                                                                               161
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                                                                                                                                                                                                                                              111 PLLWETQLGLAFLRG-LSYHDGALVVTKAGYYYIYSKVQLGGV-G-CP-L---GLAS--- 160
                                                                                                 99
                                                                                                                                                                                                  39
                                                                                                                                                                                                                                                                                               / Match 15.8%;
Local Similarity 32.1%;
nes 45; Conservative
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                                                                                              SITVVITKVTDSYPEPTQLLMGTKSVC--EVGSN--WEQPIYLGAMFSLQEGDKLMVNVS
                                                                                                                                             TITHGLYKRTPRYPEELELLVSQQSPCGRATSSSRVWWDSSFLGGVVHLEAGEEVVVRVL
                                                                                                                                                                                                ALHWEHELGLAFTKNRMNYINKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD
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RYOTA; METAZOA; CHORDATA;
  DISLVDYTKEDKTFFGAFLL
                                              DERLVRLRDGTRSYFGAFMV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISLYDYTKEDKTFFGAFLL
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  174
                                                                                                                                                                                                                                                                                               Score 208; DB 4;
Pred. No. 4.26e-21;
38; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 216; DB 4;
Pred. No. 1.06e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                               Length 240,
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SPEAR
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Best Local Similarity
Matches 39; Conser
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPRA HIRCUS (GOAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
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HARRISON G.A., BROUGHTON M.J., DEANE E.M.,
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ I
EMBL; AF055915; G3659513; -
PROSITE; PS00251; TNF_1; 1.
SEQUENCE 233 AA; 25696 MW; 5B4C4E1E CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDAT
TUMOUR NECROSIS FACTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ EMBL; D86587; D1013817; --
PROSITE; PS00251; TNF_1; 1.
PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAKAKURA H., MORI Y., TATSUMI M.;
"Molecular cloning of caprine TNF-alpha
E.coli and insect cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               028320;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 LQWLKRRANVLLSNGMDLVDNQLVVPSTGLYLVYSQLLFKG--EDCANEPLL-LTHTVSR 158
  219
                                                100
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                                                                                                                                                                           LRWGDSYANALKANGVELKDNQLVVPTDGLYLIYSQVLFRG-HG-CPSTPLF-LTHTISR 159
LDYAESGQVYFGIIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDFAESGOVYFGVIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VALSYQSKVNLLSAIKSPCQKTVKGARE-ASPWYEPIYLGGVFQLEKGDKLSADTNYPNY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
                                                ITVVI-TKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISL
                                                                                           IAVSYQTKVNILSAIKSPCHRETPEGAE-AKPWYEPIYQGGVFQLEKGDRLSAEINQPEY 218
                                                                                                                                             LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
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                                                                                                                                                                                                                                                                                                                                                234 AA;
                                                                                                                                                                                                                                           15.2%;
larity 28.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                             25519 MW;
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31; M
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                                                                                                                                                                                                                                                                                                                                             C6424744 CRC32;
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                                                                                                                                                                                                                                                                    200; DB 6;
No. 1.66e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203; DB 6;
No. 4.21e-20;
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                                                                                                                                                                                                                                             61; Indels
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                                                                                                                                                                                                                                                                                           Length 234;
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                                                                                                                                                                                                                                                                                                IMMUNOGENETICS 45:459-461(1997).
EMBL; U68414; G2304957; -.
PROSITE; PS00255; TNF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
TUMOR NECROSIS FACTOR ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JANG J.S., KIM B.E.;
SUBMITTED (JAN-1998) TO EMBI
EMBL; AF043342; G2905634; --
PROSITE; PS00251; TNF_1; 1.
                                                                                                                                                                                                                                                                                  PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 97246744.
IRAQI F., TEALE A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A/J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035853;
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01-JUN-1998 (TREMBLREL. 06,
01-JUN-1998 (TREMBLREL. 06,
TUMOR NECROSIS FACTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         043647;
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and sequencing of the tnfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
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       160
                                                                                   102 LEWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQVLFKGQ-G-CPDYVLLTHTVSRFA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159
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                                                                                                                                                     Local Similarity nes 37; Conser
                                                 40 LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ-G-CPST-HVLLTHTISR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 38; Conser
ISYQ-EKVNLLSAVKSPCPKDTPEGAELKP-WYEPIYLGGVFQLEKGDQLSAEVNLPKYL 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAVSYQTKVNLLSAIKSPCQRETPRGAE-AKPWYEPIYLGGVFQLEKGDRLSAEINRPDY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
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                                                                                                                                                                                                                                                      PF00229; TNF;
NCE 232 AA;
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                                                                                                                                                  14.4%;
llarity 27.4%;
Conservative
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                                                                                                                                                                                                                                                   25513 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.52e-18;
34; Mismatches 59
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LAST ANNOTATION UPDATE)
(FRAGMENT).
                                                                                                                                                  Score 189; DB 11;
Pred. No. 2.39e-17;
34; Mismatches 60
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                                                                                                                                                                                                                                                      9B2B3F06 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                     60;
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                                                                                                                                                                                                 Length 232;
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Best Local
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                                                                                                                                                                                    Q62326 PRELIMINARY;
Q62326;
Q1-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
TUMOR NECROSIS FACTOR.
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01-JAN-1998 (TREMBLREL 05,
01-JAN-1998 (TREMBLREL 05,
01-NOV-1998 (TREMBLREL 08,
TUMOR NECROSIS FACTOR ALPHA
                                                                                                                                       MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PERIPHERAL BLOOD;
ZHOU H., HU J., SEEGER C.;
SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARMOTA MONAX (WOODCHUCK).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
CERAMI A.;
                      CAPUT D.,
                                          SEQUENCE FROM N.A. MEDLINE; 86149365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98139533.
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                                                                                                                     SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOHRENGEL B., LU M., ROGGENDORF M.;
"Molecular cloning of the woodchuck
                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMUNOGENETICS 47:332-335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 LVWLSRRANALLANGMELIDNQLVVPANGLYLVYSQVLFKGQGCPSYVLLTHTVSRFAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 YLDFAESGQVYFGVIAL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMT-SECSEIRQA-GRPNKP
                                                                                                                                                                                                                                                                                                                                                                                                              LVDYTKEDKTFFGAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YQDKVNLLSAIKS-PCPKESLEGA----EFKP-WYEPIYLGGVFELQKGDRLSAEVNLPS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFAESGOVYFGVIAL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSITVVITKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITVVITKVIDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 13.6%;
Similarity 29.9%;
41; Conservative
                         BEUTLER B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCIURIDAE; SCIURINAE;
                                                                                                                     MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 I
233 I
25764 MW;
                         HARTOG
                                                                                                                     MURINAE;
                                                                                                                                                                                                               01,
                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 179; DB 11;
Pred. No. 2.04e-15;
33; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
PRECURSOR.
                         ×.
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                                                                                                                     VERTEBRATA;
E; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6FC0F34A CRC32;
                         THAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokines: TNF-alpha, IFN-gamma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARMOTA
                                                                                                                                                                                                                                                                                                                 156
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                         70
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                                                                                                                                            MAMMALIA;
                         BROWN-SHIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; RODENTIA;
                                                                                                                                            EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                            RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local :
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Best I
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                              O14788;
O14788;
O1-JAN-1998
O1-JAN-1998
O1-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                      LT 10
1770 PRELIMINARY; PRT; 233 AA.
O18779; O1-JAN-1998 (TREMBLREL 05, CREATED)
O1-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
 OMOH
                                                                                                                                                                                                                                                                                                 SUBMITTED (JUL-1997) TO EMB
EMBL; AF011926; G2599343; -
PROSITE; PS00251; TNF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                               BOS TAURUS (BOVINE).

BOS TAURUS (BOVINE).

CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a co
3'-untranslated region
mediators.";
                     RANKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M13049; E7693; -. PROSITE; PS00251; TNF_1; 1. PFAM; PF00229; TNF; 1.
          RANKL
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-N'DAMA;
                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS
                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         ARTIODACTYLA; RUMINANTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                        TRAQI F.
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 SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFAESGQVYFRVIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISYQ-EKVNLLSAVKSPCPKDTPEGAELKP-WYEPIYLGGVFQLEKGDQLSAEVNLPKYL 141
                                                                                                                VDYTKEDKTFFGAFLL
                                                                                                                                  LDYAESGOVYFGIIAL
                                                                                                                                                       ITVVI-TKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISL
                                                                                                                                                                          IAVSYQTKVNILSAIKSPCHRETPEWAE-AKPWYEPIYQGGVFQLEKGDRLSAEINLPDY
                                                                                                                                                                                               LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYTKEDKTFFGAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITVVITKYTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLV
                                                                                                                                                                                                                                                                                        PF00229; TNF;
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 36; Conser
                              (TREMBLREL.
(TREMBLREL.
                                                                                                                                                                                                                                                                               233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 AA; 17357 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAD. SCI. U.S.A. 83:1670-1674(1986).
                                                                      PRELIMINARY;
 (HUMAN)
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  FACTOR ALPHA
                                                                                                                                                                                                                                                                       25395 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%;
                                                                                                                                                                                                                                                 13.3%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
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                                                                                                                                                                                                                                                                                                                       TO EMBL/GENBANK/DDBJ
                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ommon nucleotide sequence in to of mRNA molecules specifying
                               866
                                                                                                                                                                                                                                                                                                                                                                         ATA; VERTEBRATA; MAMMALIA; PECORA; BOVOIDEA; BOVIDAE;
                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 177; DB 11;
Pred. No. 4.93e-15;
34; Mismatches 61
                                                                                                                                                                                                                                     Score 175; DB 6;
Pred. No. 1.19e-14;
30; Mismatches 62
                                                                                                                                                                                                                                                                               64FAFC88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03975542 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 61;
                                                                       317
                                                                                                                                                                                                                                                                               CRC32;
                                                                      A
                                                                                                                                                                                                                                                                                                                        DATA
                                                                                                                                                                                                                                                                                                                                                                          BOVIDAE;
                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                                                                          Length 233;
                                                                                                                                                                                                                                                                                                                        BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA;
; BOVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
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Best Local S
Matches
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Best Local
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                                                                                                                                                                                                                                                                    014723
014723;
014723;
01-JAN-1998
01-JAN-1998
01-JOV-1998
                                                                      NON_TER
SEQUENCE
                                                                                          "TRANCE is a novel ligand of the tumor necrosi family that activates c-Jun N-terminal kinase J. BIOL. CHEM. 272:25190-25194(1997). EMBL; AF013171; G2411500; -. PFAM; PF00229; TNF; 1
                                                                                                                                                                 MEDLINE; 97460112.
WONG B.R., RHO J., ARRON J., ROBINS
KALACHIKOV S., CAYANI E., BARTLETT
                                                                                                                                                                                                                                    TRANCE (FRAGMENT).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF019047; G2612922;
EMBL; AF053712; G3057146;
PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation and a CELL 93:165-176(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BURGESS T.,
SULLIVAN J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 98227661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDERSON D.M., MARASKOVSKY
TOMETSKO M.E., ROUX E.R., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; CATARRHINI; HOMINIDAE; HOMO. [1]
                                                                                                                                                       CHOI Y.;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                          CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOYLE W.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LACEY D.L., TIMMS E., TAN H.-L., KELLEY M.J., BURGESS T., ELLIOTT R., COLOMBERO A., ELLIOT SULLIVAN J., HAWKINS N., DAVY E., CAPPARELLI C KAUFMAN S., SAROSI I., SHALHOUB V., SENALDI G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and dendritic-cell functi
NATURE 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A homologue of the
 115
                                                                                                                                                                                                                                                                                                                                                                                                                   102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Osteoprotegerin ligand is a cytokine
                                                                                                                                                                                                                                                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
WYHDRGWG-KISNMTFSNGKLIVNQDGFYYLYANICFRHHETS-GDL--AT-EY-LQ-LM
                                                                                                                                                                                                                                                                                                                                                                                           D-PDQDATYFGAF 311
                                                                                                                                                                                                                                                                                                                                                                                                                 VVITKVTDSYPEPTQLLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLMVNVSDISLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSIT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WYHDRGWA-KISNMTFSNGKLIVNQDGFYYLYANICFRHHETS-GDL--AT-EY-LQ-LM 239
                                                                                                                                                                                                                                                                                                                                                                     DYTKEDKTFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                         VYYTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                   Similarity
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                                                                                                                                                                                                                                                                       8 (TREMBLREL.
8 (TREMBLREL.
                                                                    245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA;
                      11.7%;
larity 27.1%;
Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35478 MW;
                                                                      27804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activation.";
                                                                                                                                                                                                                                                                        86,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y E., B
                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 157; DB 4;
Pred. No. 2.78e-11;
36; Mismatches 50
                      Score 154; DB 4;
Pred. No. 9.83e-11;
37; Mismatches 50
                                                                                                                                                                  ROBINSON E.,
                                                                                                                                                                                                                                     VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BILLINGSLEY W.
E M.C., DUBOSE
                                                                      F7CD1ECE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A58E6DC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLEY M.J., DUNSTAN C.R.,
ELLIOTT G., SCULLY S., HSU H.,
APPARELLI C., ELI A., QIAN Y.-X.,
SENALDI G., GUO J., DELANEY J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            its
                                                                                                                                                                                                                                                                                                                      245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that regulates osteoclast
                                                                                                                                            necrosis
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                                                                                                                                                                  ORLINICK J., CHAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.F., COSMAN D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 317
                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enhance T-cell growth
                       Indels
                                                                                                                                 cells
                                                                                                                                                                                                                                       EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA; PRIMATES;
                                                                                                                                                                             CHAO
                       10;
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                       Gaps
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                                                                                                                                                                  S.Y.,
 167
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RESULTANDO ACCOMENTANTO ACCOMEN
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Best Local S
Matches 3
                                           SEQUENCE FROM N.A.
MEDLINE; 98032977.
ANDERSON D.M., MARASKOVSKY E., I
TOMETSKO M.E., ROUX E.R., TEEPE
GALIBERT L.;
                                                                                                                                                                                                                                                                                                                                                                                           035306;
035306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
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MESOCRICETUS AURATUS (GOLDEN HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98234044.

MELBY P.C., TRYON V.V., CHANDRASEKAR B., FREEMAN G.L.;

MELBY P.C., TRYON MESTER (Mesocricetus auratus) cytokine cDNAs analysis of cytokine mRNA expression in experimental visceral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TREMBLREL 07, 01-AUG-1998 (TREMBLREL 07, 01-NOV-1998 (TREMBLREL 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              070332
                                                                                                                                                                                               SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                      TRANCE OR RANKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    070332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leishmaniasis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
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homologue of the dendritic-cell f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYT::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEWLSHRANALLANGMSLKDNQLVIPADGLYLVYSQVLFRGQ-G-CPSYVLLTHTVSRIA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITVVITKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSYE-DNVNLLSAIKSPCPKETPEGEELKP-WYEPIYLGGVFQLEKGDRLSAEVNLPKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYTKEDKTFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-PDQDATYFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVITKVTDSYPEPTQLLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLMVNVSDISLV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r. IMMUN. 66:2135-2142(1998).
AF046215; G3005109; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6%;
Similarity 27.6%;
34; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00251; TNF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172
  function
                 INF receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRICETINAE; MESOCRICETUS
                                                                                                                                                                                            MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 152; DB 11;
Pred. No. 2.27e-10;
31; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UP
LAST ANNOTATION
                                                                    BILLINGSLEY W.L., DO E M.C., DUBOSE R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79A08367 CRC32;
                                                                                                                                                                                               SUM
                      its ligand
                                                                                                                                                                                                                                                                                                                                                                                                                     316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 AA
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                                                                                                                                                                                                                   MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 216;
                      enhance T-cell growth
                                                                    COSMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                   EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
                                                                                              Σ
                                                                    W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
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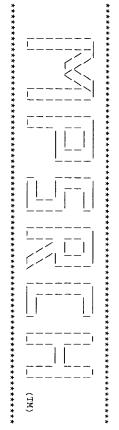
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       ALD DOT REPORT OF THE PROPERTY OF THE PROPERTY
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Best Local S
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 390:175-179(1997).
EMBL; AF019048; G2612924; -
MGD; MGI:1100089; TRANCE.
PFAM; PF00229; TNF; 1.
SEQUENCE 316 AA; 35002 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      035235;
01-JAN-1998
01-JAN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 15
035235
                            MGD; :
                                                                           PROC. NATL. ACAD. SCI. U.S.A. EMBL; AF053713; G3057148; ... EMBL; AF013170; G2411498; ... EMBL; AB008426; D1026353; ...
                                                                                                                                                                         YASUDA H., SHIMA N., NAKAGAWA N., YAMAGUCHI K., KINOSAKI M., MOCHIZUKI S., TOMOYASU A., YANO K., GOTO M., MURAKAWI A., TSUDA MORINAGA T., HIGASHIO K., UDAGAWA N., TAKAHASHI N., SUDA T.; "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is iden to TRANCE/RANKL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Osteoprotegerin ligand is a cytokine that differentiation and activation."; CELL 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LACEY D.L., TIMMS E., TAN H.-L., KELLEY M.J., DUNSTAN C.R.,
BURGESS T., ELLIOTT R., COLOMBERO A., ELLIOTT G., SCULLY S., HSU
SULLIVAN J., HAWKINS N., DAVY E., CAPPARELLI C., ELI A., QIAN Y.
KAUFWAN S., SAROSI I., SHALHOUB V., SENALDI G., GUO J., DELANEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHOLT:
"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. BIOL. CHEM. 272:25190-25194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 97460112.
WONG B.R., RHO J., ARRON J.,
KALACHIKOV S., CAYANI E., BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 98227661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                    MEDLINE; 98188248
                                                                                                                                                                                                                                                                                                                                                         TISSUE=BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOYLE W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42
MGI:1100089; TRANCE.; PF00229; TNF; 1.
ENCE 316 AA; 34944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSIT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WYHDRGWA-KISNMTLSNGKLRVNQDGFYYLYANICFRHHETS-GSV-PTD--Y-LQ-LM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYTKEDKTFFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-PDQDATYFGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVITKVTDSYPEPTQLLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLMVNVSDISLV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 35; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION-INDUCED CYTOKINE (TRANCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%;
larity 26.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35002
       34944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.6
       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J., ROBINSON E., ORI
BARTLETT F.S. III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQ
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Pred. No. 1.71e-06;
33; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                       95:3597-3602(1998).
     F76EC806 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97DA4504 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulates
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Query Match

Score

DB

Length



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 18 13:20:29 2000; MasPar time 6.81 Seconds 722.274 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-09-246-129-2 (1-174) from US09246129A.pep 1314 1 MRRFLSKVYSFPMRKLILFL......DISLVDYTKEDKTFFGAFLL 174

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 l:swissprot

Statistics: Mean 45.305; Variance 75.582; scale 0.599

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB.	ID	Description	Pred. No.
1	242	18.4	202	<u>ا</u> بر	TNFB_RAT	LYMPHOTOXIN-ALPHA PREC	4.89e-29
2	241	18.3	202	۳	TNFB_MOUSE		.00e-
ω	235	17.9	291	Ľ	TRAI_MOUSE		
4	232	17.7	279	_	FASL_MOUSE	FAS ANTIGEN LIGAND.	6.56e-27
տ	231	17.6	281	ш	TRAI_HUMAN	TNF-RELATED APOPTOSIS	.07e-
0	229	17.4	197	┙	TNFB_RABIT		.83e-2
7	229	17.4	204	Ц	TNFB_BOVIN		2.83e-26
80	220	16.7	281	-	FASL_HUMAN		.20e-2
9	217	16.5	204	\vdash	TNFB_PIG	-ALPHA P	.32e-2
10	212	16.1	278	H	FASL_RAT	FAS ANTIGEN LIGAND.	.02e-2
11	200	15.2	205	Н	TNFB_HUMAN	LYMPHOTOXIN-ALPHA PREC	.00e-2
12	200	15.2	233	ب	TNFA_MACFA	TUMOR NECROSIS FACTOR	.00e-2
13	198		233	Ъ	TNFA_TRIVU		.68e-2
14	197	15.0	233	\vdash	TNFA_MACMU	NECROSIS	1.23e-19
15	197	15.0	233	-	TNFA_PAPHU		1.23e-19
16	196	14.9	193	ш	TNFA_CAPHI	TUMOR NECROSIS FACTOR	1.96e-19
17	196	14.9	232	Ц	TNFA_PIG		1.96e-19
18	194	14.8	233	Ц	TNFA_HUMAN		.98e-
19	191	14.5	233	ب	TNFA_PAPSP		.01e-
20	191	14.5	233	μ	TNFA_CANFA	TUMOR NECROSIS FACTOR	.01e-
. 21	191	14.5	306	\vdash	TNFC_MOUSE	OTOXIN-BET	2.01e-18
22	189	14.4	234	Н	TNFA_SHEEP	TUMOR NECROSIS FACTOR	.07e-
23	189	14.4	235	Ц	TNFA_MOUSE	TUMOR NECROSIS FACTOR	.07e-1

M.

Query Match 18.4%; Best Local Similarity 36.5%;

Score 242; DB 1; Length 202; Pred. No. 4.89e-29;

22 20 30 30 30 30 30 30 30 30 30 30 30 30 30	24 25 26 27
176 175 171 169 138 101 100 98 97 96 97 98 97	187 187 184 181
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233 2233 2233 2233 2344 3384 2552 2552 2667 2667 2667 2677 2677 2677	234 234 235
TNFA_RAT TNFA_BOVIN TNFA_CEREL TNFA_FELCA TNFC_HUMAN RCI2_ECOLI RCI1_ECOLI RCI1_ECOLI CO14_BCOUN CI74_BCOUN CN24_HUMAN CN24_HUMAN CN41_MOUSE VI_2_HPV48 NAH1_CRIGR VIZ_HPV48 BNAH1_CRIGR MEN3_YEAST MET3_YEAST FIXN_AZOCA BRM_DROME	TNFA_HORSE TNFA_PERLE TNFA_CAVPO TNFA_RABIT
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MEDLINE; 87224127.
LI C.B., GRAY P.W.,
RUDDLE N.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRAY P.W., CHEN E., TANG W.-L., RUDDLE N.;
"The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.
NUCLEIC ACIDS RES. 15:3937-3937(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LITA UK ANALIS (MOUSE).

MUS MUSCULUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;

EUKARYOTA; MITAZOA; CHORDATA; MURIDAE; MURINAE;
SEQUENCE OF 56-76 FROM N. MEDLINE; 91042516. WEIL D., BROSSET S., DAUT
                                                                                                                                                                                                                    GARDNER S.M., MOCK B.A., HILGERS J., HUPPI K.E., ROEDER W.D.; "Mouse lymphotoxin and tumor necrosis factor: structural analysis the cloned genes, physical linkage, and chromosomal position."; J. IMMUNOL. 139:476-483(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDOSPASOV S.A., HIRT B., SHAKHOV A.N., DOBRYNIN V.N., KAWASHIMA ACCOLLA R.S., JONGENEEL C.V.;
"The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are tandemly arranged on chromosome 17 of the mouse.", NUCLEIC ACIDS RES. 14:7713-7725(1986).
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01-NOV-1997
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                                                                        ONCOGENE
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NEDOSPASOV S.A., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEMON D., KAWASHIMA E., JONGENEEL C.V., SHAKHOV A.N., NEDOSPASOV S.A., "Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor necrosis factor) and TNF-beta (lymphotoxin) genes."; NUCLEIC ACIDS RES. 15:9083-9084(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 88067722.
                                                                                                                                                                SEQUENCE OF 6-202 FROM MEDLINE; 89144562.
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                           interferon-gamma
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                                                                                                           'Induction of tumor necrosis factor-alpha interferon-gamma mRNA by interleukin 2 in
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                                                                          RES.
                                                                                                                                                 DAUTRY F.;
                                                                                                                                                                                                                                                                                                                                                      and expression of murine OL. 138:4496-4501(1987).
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                                                                        3:409-414(1988).
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10, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
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 DAUTRY F.;
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Query Match
Best Local
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01-OCT-1996
01-OCT-1996
01-NOV-1997
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
COTTECCNATHI; MURIDAE; MURINAE;
                                                                                                                             TNF-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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CYTOKINE; GLYCO
                   SEQUENCE
                                                                                                                                                                                                                       TRAI_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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700467; G54833; -...

700467; G54839; -...

706217; G54839; -...

706218; E7696; -...

704800; G736269; -...

704800; G736269; -...

70556; G202001; -...

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705619; G2020089; -...
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                   FROM N.A.
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PS50049; TNF_2;
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104797; LTA
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202 AA;
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(REL. 35, LAST ANOTATION UPDAT
APOPTOSIS INDUCING LIGAND (TRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 8.00e-29;
22; Mismatches 57
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                                                                                                                                             UPDATE)
                                                                                                                           (TRAIL PROTEIN)
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                                                     MAMMALIA; EUTHERIA; MUS.
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Best Local
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01-FEB-1995
15-JUL-1998
                                                                                                                                         SUDA T., NAGATA S.;
"Generalized lymphoproliferative mutation in the Fas ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                     FAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00251; TNF_1;
PROSITE; PS50049; TNF_2;
PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles remained a long as its content.
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-!- SUBUNIT: HOMOTRIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
-!- TISSUE SPECIFICITY: WIDESPREAD.
-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILEY S.R., SCHOOLEY K., SMOLAK P.J., DIN W.S., HUANG C.-P., NICHOLL J.K., SUTHERLAND G.R., DAVIS-SMITH T., RAUCH C., SMITH C.A., GOODWIN R.G.;
MEDLINE; 95388076.
PEITSCH M.J., TSCH
                                              STRAIN=C57BL/6;
                                                                                                                CELL 76:969-976(1994).
                                                                                                                                                                                                             TAKAHASHI T.,
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 94185175.
                                                                                                                                                                                                                                                                                                                              EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FASL_MOUSE
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IMMUNITY 3:673-682(1995).
                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                        RODENTIA; SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                            APTILGI OR FASL OR GLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P41047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216
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                                                                                                                                                                                                                                                                                                                    JS (MOUSE).
METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                      (REL. 31, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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TSCHOPP J.J.;
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31.4%;
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                                                                      3D-STRUCTURE
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Pred. No. 1.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                               disease
                                                                    MODELLING
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                                                                                                                                                                                                           JENKINS
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Best Local
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CARBOHYD
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ROUSSEAU M., BRON C., RENNO T., FRENCH L., TSCHOPP J.;
"Characterization of the non-functional Fas ligand of gld mice.";
INT. IMMUNCL 7:1381-1386(1995).
-!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The mouse Fas-ligand gene
TNF family gene cluster.";
IMMUNITY 1:131-136(1994).
                                                                                     SEQUENCE
                                                                                                                              CARBOHYD
                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                    PFAM; PF00229; TNF; 1. HSSP; P01375; 2TUN.
                                                                                                                                                                                                                                                                                                                              PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:99255; FASL.
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                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYNCH D.H., WATSON M.L., ALDERSON M.R., TOUGH T., GIBSON M., DAVIS-SMITH T., SM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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of the TNF family.";
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                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SURFAC
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SUBUNIT: HOMOTRIMER (PROBABLE)
SUBCELLULAR LOCATION: TYPE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTO THE
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                             Similarity 54; Conser
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279
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101
4
45
200
273
                            17.7%;
larity 35.3%;
Conservative
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                                         Score 232; DB 1;
Pred. No. 6.56e-27;
                                                                                                              ITS RECEPTOR POTENTIAL.
POTENTIAL.
POTENTIAL.
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SIGNAL-ANCHOR (TYPE-II ME
EXTRACELLULAR (POTENTIAL)
                                                                                                  POTENTIAL
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BY SIMILARITY.
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                                                                                   CRC32;
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BY CLEAVAGE FORM THE CEL
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                                                                                                                                                                        ABOLISH
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                                                                                                                                                                                                                                             MEMBRANE PROTEIN).
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P50591;
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01-OCT-1996
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILEY S.R., SCHOOLEY K., NICHOLL J.K., SUTHERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: INDUCES APOPTOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASHKENAZI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PITTI R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOODWIN R.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNF-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOKINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of a new member of the TNF family that induces apoptosis.";
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMUNITY 3:673-682(1995).
                                                                                                                                         154 WESSRSGHSFLSN-LHLRNGELVIHEKGFYYIYSQTYFR-FQ-E--EIKENTKNDK-QMV 207
  101
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                                                                                                            42
                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
  TVVITKVTDSYPEPTQLLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLMVNVSDISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTK-SVCEVGSNWFQPIYLGAMF 141
                                                QY-IYKYT-SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHL 265
                                                                                                            WEHEL-GLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U37518; G1149558; -. U57059; G1336208; -.
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                                                                                                                                                                                                                                                                                                                                    281 AA;
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(REL. 34, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN) (APO-2 LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MARSTERS S.A., RUPPERT S., DONAHUE C.J., MOORE
                                                                                                                                                                                                                         Conservative
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38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMOLAK P.J., DIN W.S., G.R., DAVIS-SMITH T.,
                                                                                                                                                                                                                                                                                                                                      M.
                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                Score 231;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                      DB 1;
.07e-26;
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C., SMITH C.A.,
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHAKHOV A.N., KUPRASH D.V., TURETSKAYA R.L., AZIZOV M.M.,
ANDREYEVA A.V., NEDOSPASOV S.A.;
"Cloning and structural analysis of genes coding for tumor necrosis
factor and lymphotoxin in rabbits.";
MOL. BIOL. (MOSK) 23:1743-1750(1989).
-!- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES WHICH
IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITRO AND IN VIVO.
-!- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNITS
OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.
-!- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTA OR THEE.
ORYCTOLAGUS CUNICULUS (RABBIT).
ORYCTOLAGUS CUNICULUS (RABBIT).
MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; PN0098; PN0098.

PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2; PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X55745; G297168; ALT_SEQ.
EMBL; M60340; G165755; -.
EMBL; M60341; G155758; -.
PIR; JH0309; JH0309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of the rabbit TNF locus, containing the encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOKINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 90220566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 ID-MDHEASFFGAFLV
                                                         122 YLAHEVQLFSSQYSFHVPLLSAQKSVCPGPQGPWVRSVYQGAVFLLTQGDQLSTHTDGIA 181
      99
                                                                                                                                                    68 SLRWRANTDRAFLRHGFSLSNNSLLVPSSGLYFYYSQVVFSG-EG-CSP-K-AV-PT-PL 121
                                                                                                                      39 ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
   SITYVITKVTDSYPEPTQLLMGTKSVCEVG-SNWFQPIYLGAMFSLQEGDKLMVNVSDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDYTKEDKTFFGAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOPROTEIN; CYTOTOXIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                      88
197 AA;
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19, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                              17.4%;
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21126
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                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                   Score 229; DB 1; Le Pred. No. 2.83e-26; 27; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                        POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                LYMPHOTOXIN-ALPHA
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Best Local S
Matches 4
  FASL_HUMAN
P48023;
01-FEB-1996
01-FEB-1996
15-DEC-1998
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01-JUN-1994 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLUDTS I., CLEUTER Y., KETTMANN R., BURNY A., DROOGMANS L.;
"Cloning and characterization of the tandemly arranged bovine
lymphotoxin and tunour necrosis factor-alpha genes.";
CYTOKINE 5:336-341(1993).

-i- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES WHICH
IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITRO AND IN VIVO.

-i- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNITS
OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTA OR TNFB.

BOS TAURUS (BOVINE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                         CYTOKINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                    œ
                                                                                                           LVDYTKEDKTFFGAFLL
                                                                                                                                                                                   YLAHEVOLFSPOYPFHVPLLSAOKSVCPGPOGPWVRSVYOGAVFLLTRGDOLSTHTDGIS 188
                                                                                                                                                                                                             ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD 98
                                                                                                                                                                                                                                     SLRWRANTDRAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGR-G-CFP-R-AT-PT-PL 128
                                                                                                                                                                                                                                                                                                                                                                                                                              S24641; S24641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                  HL-LLSPSSVFFGAFAL 204
                                                                                                                                                           SITVVITKVTDSYPEPTQLLMGTKSVCEVG-SNWFQPIYLGAMFSLQEGDKLMVNVSDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Z14137; G797; -.
                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
94083525.
                                                                                                                                                                                                                                                                                                                                                                                                PS00251; TNF_1; 1.
PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN; CYTOTOXIN; SIGNAL.

1 33 BY SIMILARITY.
    (REL.
(REL.
                                                                                                                                                                                                                                                                                                                       204 AA;
                                                                                                                                                                                                                                                                                                                                  34
95
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                        TNF;
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29, CREATED)
29, LAST SEQU
35, LAST ANNO
33, CREATED)
33, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRECURSOR (LT-ALPHA)
                                                                                                                                                                                                                                                                              17.4%;
                                                                                                                                                                                                                                                                                                                       22098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                           174
                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                                                  Score
Pred.
23; M
                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                               LYMPHOTOXIN-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                    E0B38524 CRC32;
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                             229; DB 1;
No. 2.83e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOVOIDEA;
                                                      281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TNF-BETA).
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                                                      ΑA
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                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOVIDAE;
                                                                                                                                                                                                                                                                                          Length 204;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOS.
                                                                                                                                                                                                                                                                Gaps
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WILKINSON J.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
DOMAIN
DISULFID
                         DOMAIN
DOMAIN
                                                                                                                                                                        EMBL;
                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKAHASHI T., TANAKA M., INAZAWA J "Human Fas ligand: gene structure, specificity.";
                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 95071350.
MITA E., HAYASHI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. SCHAETZLEIN C.E., POE SUBMITTED (JUN-1995)
                                                                                                                                  PROSITE; PS00251; INF_1; PROSITE; PS50049; INF_2;
                                                                                                                                                              MIM; 134638;
                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 95105731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL) APT1LG1 OR FASL.
                                                               DOMAIN
                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOCHEM. BIOPHYS. RES. COMMUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUSAMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 95127560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALDERSON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMATES; CATARRHINI;
                                                     TRANSMEM
                                                                              DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Role of Fas ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Fas ligand mediates activation-induced cell death
                                                                                                                                                                                                                                                                                                                                                                                     T CELLS, OR BOTH.
SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
SUBCELLULAR TOTAL THE CELL PROBABLY BY CLEAVAGE FORM THE CELL
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE T CELLS, OR BOTH.
                                                                                                                                                                       x89102; G887456; -..; U08137; G624628; -..; U11821; G59543; -..; D38122; G1169902; -..; 296050; E320286; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMUNOL.
                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                         P01375; 2TUN
                                                                                                                       PF00229;
                                                                               MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H., KAMADA
                                                                                            TRANSMEMBRANE;
1
81
103
4
45
202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6:1567-1574(1994).
                                                                                                                     TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POEHLMANN R.,
80
102
281
70
65
233
                                                                                                                                                                                                                                                                   tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHLMANN R., PHILIPPSEN P., EIBEL TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s.,
                                                                                            GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INAZAWA J., ABE T., SUDA T., NAGATA structure, chromosomal location and s
POLY-PRO.
BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAKEHARA T.,
                                    SIGNAL-ANCHOR
EXTRACELLULAR
                                                                 CYTOPLASMIC
                          PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204:468-474(1994).
 SIMILARITY
                                                                                          SIGNAL-ANCHOR;
                                                                                                                                                                                                                                                                                                              There are no restrictions on
                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIJIOKA T., KASAHARA
                                                 (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE FORM THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ĺ'n
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                                                                                            APOPTOSIS
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RESULT OF COMPANY AND COLOR CO
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                                                                  Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                     CYTOKINE; GLYCOPROTEIN; CYTOTOXIN; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENE 102:171-178(1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comparative analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KUHNERT P., WUETHRICH C., PETERHANS E., PAUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91340150.
KUHNERT P., WUETHRICH C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFB_PIG
                                                                                                                                                                                                                                                                             PFAM; PF00229;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; X54859; G2133; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARTIODACTYLA; SUIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 PLEWEDTYGIVLLSG-VKYKKGGLVINETGLYFVYSKVYFRGQ-S-CNNLPLS---HK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 LVDYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES WHICH IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITO AND IN VIVO. SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNITS OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                S17289; S17289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVNF-EESQTFFGLYKL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SITYVITKVTDSYPEPTQLLMGTK-SVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDIS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VYM-R-NSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                     Similarity 45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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250
260
281
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                                                                  16.5%;
ilarity 32.8%;
Conservative
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                                                                                                                                                                                                                                                                                TNF;
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95 P
21960 MW;
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35.8%;
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                                                                  Score 217; DB 1; Le
Pred. No. 9.32e-24;
25; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
30; 1
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                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                        LYMPHOTOXIN-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                             1127B71C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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FAS ANTIGEN LIGAND.
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PROSITE; PS00251; TNE_1;
PROSITE; PS50049; TNE_2;
PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUDA T., TAKAHASHI T., GOLSTEIN P., NAGATA S.; "Molecular cloning and expression of the Fas ligand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                        CYTOKINE;
                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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RODENTIA; SCIUROGNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APT1LG1 OR FASL.
                           SEQUENCE
                                                                   CARBOHYD
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                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 HL-LLSPSSVFFGAFAL 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the tumor necrosis factor family.";

11.75:1159-1178(1993).

FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.

FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
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T CELLS, OR BOTH.

SUBUNIT: HOMOTRIMER (PROBABLE).

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY

SUBCELLULAR FLUID, PROBABLY BY CLEAVAGE F
                                                                                                                                                                                                                                                                                                                                                                                                                                          SURFACE.
TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES
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(REL. 29, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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                           31140 MW;
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 Score 212;
                         POTENTIAL. POTENTIAL. 6DC17725
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                            OPROTEIN; SIGNAL-ANCHOR; APOPTOSIS.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                           POTENTIAL.
                                                                                                                        BY SIMILARITY.
                                                                                                                                     POLY-PRO
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AE; MURINAE; RATTUS.
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NEDWIN G.E., JARRETT-NEDWIN J., SMITH D.H.
                                                                                                        MATSUYAMA N., OKAWA N., TSUKII Y., ENDO T., KAJI A.; "Nucleotide sequence of a cDNA encoding human tumor necrosis beta from B lymphoblastoid cell RPMI 1788."; FEBS LETT. 302:141-144(1992).
                                                                                                                                                                                                                                                                              PALLADINO M.A., NEDWIN G.E.; "Cloning and expression of cDNA for human with tumour necrosis activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEDOSPASOV S.A. SHAKHOV A.N., TURETSKAYA R.L., METT V.A., AZIZOV M.M., GEORGIEV G.P., KOROBKO V.G., DOBRYNIN V.N., FILLPPOV S.A., BYSTROV N.S., BOLDYREVA B.F., CHUVPILO S.A., CHUMAKOV A.M., SHINGAROVA L.N., OVCHINNIKOV Y.A.;
  MEDLINE; 93272029.
IRIS F.J.M., BOUGUELERET L.,
PERROT V., JURKA J., RODRIGU
                                                                   SEQUENCE FROM
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                NATURE 312:721-724(1984).
                                                                                                                                                                                                                                                                                                                                                   GRAY P.W., AGGARWAL B.B., JARRETT J.A., LEUNG D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOBAYASHI Y., MIYAMOTO D., ASADA "Cloning and expression of human human T cell hybridoma.";
J. BIOCHEM. 100:727-733(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tandem arrangement of genes coding for tumor necrosis factor alpha) and lymphotoxin (TNF-beta) in the human genome.";
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EUKARYOTA; METAZOA; CHORDATA;
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01-NOV-1997
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    RODRIGUEZ-TOME
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LAST ANNOTATION UPDATE)
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MOFFAT B., N
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AE; HOMO.
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lymphotoxin mRNA
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Mismatches 44;
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3 P., SVEDERSKY
  CATERINA
CLAVERIE
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                                                                                                                                                                                                                                                                                                      lymphotoxin,
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L.P.,
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABRAHAM L.J., DU D.C., ZAHEDI K., DAWKINS R.L., WHITEHEAD A.S.;
"Haplotypic polymorphisms of the TNFB gene.";
"IMMUNOGENETICS 33:50-53(1991).
-!- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES W
IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITRO AND IN
-!- SUBUNIT: HETEROTRINER OF EITHER TWO BETA AND ONE ALPHA SUBUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COHEN D.;
"Dense Alu clustering and a potential family within a 90 kilobase HLA class NAT. GENET. 3:137-145(1993).
                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                            the
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                                                                                                                                                                           CHAIN
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           130
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                              39
                                                   76
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                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR (LESS PREVALENT) TWO ALPHA AND ONE BETA
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; A06316;
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                              ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD 98
                                                SLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKA--YSP-K-AT-SS-PL
                                                                                                                                                                                                                                              A26085; QWHUX.
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M55913;
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M16441;
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                                                                                                                                                                                              GLYCOPROTEIN;
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                                                                      Conservative
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III segment.";
There are no
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                                                                                                                                                                                             POLYMORPHISM
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15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (
                                                                                                                                                                                     DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                           PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                       CYTOKINE;
                                                                                                                                                                                                                                                                                                                     EMBL; AB000513; G1794149; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIMATES; CATARRHINI;
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                                                                                                       102 LQWLNRRANALVANGVELTDNQLVVPSEGLYLIYSQVLFKGQ-G-CPS-NHVLLTHTISR 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: THE SOLUBLE FORM DERIVES PROTEOLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMOTRIMER.
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 LDFAESGQVYFGIIAL
                           ITVVI-TKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISL 158
                                                                              LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
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                                                  IAVSYQTKVNLLSAIKSPCQRETPEGAE-AKPWYEPIYLGGVFQLEKGDRLSAEINLPDY 217
                                                                                                                                                                                                                                                                     PF00229; TNF; 1. P01375; 1TNF.
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233 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CERCOPITHECIDAE; CERCOPITHECINAE; MACACA
                                                                                                                                  34;
                                                                                                                                                Score 200; DB 1;
Pred. No. 3.00e-20
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
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 159
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                          218 LDFAEPGQLYFGAIAL
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                                                                                                        40 LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
                                                                             FTLSYQKKVTLLANIRSSCRKAAEDDGE-PSAWYEPVYLAGVFQLTEGDKLVVDTNYPEN 217
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"Molecular cloning and characterizatic alpha (TNF-alpha) from the Australian Trichosurus vulpecula.";
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; M
DIPROTODONTIA; PHALANGERIDAE; TRICHOSURUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (
                                                                                                                                                                                                                                                                                                                      PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).

1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
PROTEOLYTIC PROCESSING (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOL. CELL BIOL. 74:151-158(1996).

-i- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLOCK D.N., ALDWELL F.E., BUDDLE B.M.;
"Molecular cloning and characterization of tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 VDYTKEDKTFFGAFLL 174
Local Similarity
nes 38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONDITIONS (BY SIMILARITY).
SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                     $83283; G1881812; -.
AF016102; G2425046; -.
                                                                                                                                                                                                                                                                                             PF00229; TNF; 1.
                                                                                                                                                                                                                                         CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                        145
233 AA;
  Conservative
                                                                                                                                                                                                                                                                       1A8M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                   233
56
177
                           15.1%;
27.9%;
                                                                                                           25704 MW;
Pred.
                              Score 198; DB 1;
Pred. No. 7.68e-20;
                                                                                                                                 BY SIMILARITY.

TUMOR NECROSIS FACTOR.

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                           873F8626 CRC32;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    common brushtail possum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ormatics and the EMBL outst
There are no restrictions
ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAMMALIA; METATHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CACHECTIN).
  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                 Length 233;
                                                                                                                                                                                                                                         SIGNAL-ANCHOR
  Indels
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Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES,
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: HOMOTRIMER.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
EXTRACELLULAR SOLUBLE FORM.
-!- PIM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARLETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 96003435. VILLINGER F.J., BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P48094;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOKINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nonhuman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MACACA MULATTA (RHESUS MACAQUE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFA_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative sequence analysis
     159
                                                                                                                100
                                                                                                                                                                         159
                                                                                                                                                                                                                                                                             102 LQWLNRRANALLANGVELTDNQLVVPSEGLYLIYSQVLFKGQ-G-CPS-NHVLLTHTISR 158
                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nhuman primates.";
IMMUNOL. 155:3946-3954(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEOLYTIC PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND MALNUTRITION.
                                                        LDFAESGQVYFGIIAL 233
                                                                                                                                                                   IAVSYQTKVNLLSAIKSPCQRETPEGAE-AKPWYEPIYLGGVFQLEKGDRLSAEINLPDY 217
                                                                                                                                                                                                                        LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
                                                                                                             ITVVI-TKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00229; TNF; 1.
P01375; 1TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U19850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19850; G644818; -.; PS00251; TNF_1; 1; FS50049; TNF_2; 1
                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.

1 76 BY SIMILARITY.

77 233 TUMOR NECROSIS FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
145
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FACTOR PRECURSOR (INF-ALPHA) (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRAR S.S., MAYNE A.E., quence analysis of cytol
                                                                                                                                                                                                                                                                                                                                                                      15.0%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; CERCOPITHECIDAE; CERCOPITHECINAE; MACACA
                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                      Score 197; DB 1;
Pred. No. 1.23e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN). BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         146A1B48 CRC32;
                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE MEMBRANE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHIKKALA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                              Length 233;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSARI A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INCLUDING
                                                                                                                                                                                                                                                                                                                                         5
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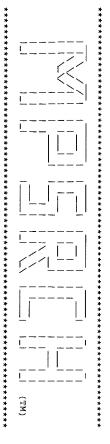
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Best Local :
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077510;
15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                               DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOL. IMMUNOL. 34:1041-1042(1997).

-!- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKING WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA)
                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                           CYTOKINE; CYTOTOXIN;
                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM PROTEOLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 98147379.
HAUDEK S.B., REDL H., SCHI
"Complementary DNA (cDNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPIO HAMADRYAS URSINUS (CHACMA BABOON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE;
159
                              218
                                                           100
                                                                                          159
                                                                                                                                                    102 LQWLNRRANALLANGVELTDNQLVVPSEGLYLIYSQVLFKGQ-G-CPS-NHVLLTHTISR
                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF CANCER AND INFECTION, AND IS CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND MALNUTRITION.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONDITIONS
VDYTKEDKTFFGAFLL 174
                            LDFAESGQVYFGIIAL
                                                           ITVVI-TKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISL 158
                                                                                        IAVSYQTKVNLLSAIKSPCQRETPEGAE-AKPWYEPIYLGGVFQLEKGDRLSAEINLPDY
                                                                                                                       LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS
                                                                                                                                                                                                                                                                                                                                                                          AF019963; G3417555;
                                                                                                                                                                                  Similarity 39; Conser
                                                                                                                                                                                                                                               145
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 37, CREATED)
(REL. 37, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                  15.0%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHORDATA;
                                                                                                                                                                                                                                               25658
                                                                                                                                                                                                                                                                                                           TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR 76 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHLAG G.,
                                                                                                                                                                                                                                                 ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                  Pred.
                                                                                                                                                                                                  Score 197;
Pred. No. 1.
                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                               E38CF6E8
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIROIR B.P.;
ce of baboon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233
                                                                                                                                                                                                    .23e-1
                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                               CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis factor
                                                                                                                                                                                                               Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASES, INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXISTS
                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outstation
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Jan

18 13:20:53 2000



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Jan 18 13:19:47 2000; MasPar time 9.89 Seconds 704.591 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

Sequence: >US-09-246-129-2 (1-174) from US09246129A.pep 1314 1 MRRFLSKVYSFPMRKLILFL......DISLVDYTKEDKTFFGAFLL 174

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.271; Variance 85.869; scale 0.516

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

. 2221144321432217322174432174321743217432	Result
242 242 232 232 229 229 220 220 217 219 196 199 189 189 189 189 187 187 187	Score
118.4 116.5 116.7	% Query Match 1
2002 2002 2002 2002 2004 2004 2005 2006 2006 2006 2006 2006 2006 2006	Length [
	DB
D270869 D270303 A53062 JH0309 JH0309 JH0309 JH0309 S2707 S17289 S26192 S26192 S26192 S26192 S26192 S26192 S26193 S	ID
tumor necrosis factor tumor necrosis factor Fas ligand - nouse tumor necrosis factor lymphotoxin - bovine Fas ligand - human tumor necrosis factor fas ligand - rat lymphotoxin alpha pre tumor necrosis factor	Description
8.30e-25 5.78e-23 2.05e-22 2.05e-22 8.93e-21 3.12e-20 3.48e-19 3.48e-19 3.49e-16 1.75e-16 1.32e-15 2.94e-15 2.94e-15 5.57e-15 6.57e-15 6.57e-15 7.17e-14 7.17e-14 7.17e-14 7.17e-15 6.57e-15 6.57e-15 6.57e-15 7.17e-14 7.17e-14	Pred. No.

ENTRY

B27303

#type complete

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω G	32	31	30	29	28	27	26	25	24
91	91	91	91	91	92	92	93	94	95	95	96	96	96	97	86	100	100	101	112	138	169
6.9	6.9	6.9	6.9	6.9	7.0	7.0	7.1	7.2	7.2	7.2	7.3	7.3	7.3	7.4	7.5	7.6	7.6	7.7	8.5	10.5	12.9
1082	745	551	511	245	822	527	3972	358	260	229	1647	1022	528	261	552	465	261	384	307	244	233
N	Ν	Ν	N	N	N	N	N	Ν	Ν	Ν	N	Ν	N	N	Ν	Ν	2	N	N	N	Ν
H70360	C70848	A55582	S55198	S48272	S30198	A38631	S75251	F69809	S21738	E70405	S45252	I53078	T00951	S53090	A64796	D69785	153476	S03815	S30432	A46066	S11688
cation efflux system	probable icd2 protein	cytochrome-c oxidase	sulfate adenylyltrans	hypothetical protein	Na+/H+-exchanging pro	transforming protein	hypothetical protein	spore germination pro	CD40 ligand - mouse	ABC transporter - Aqu	SNF2beta protein - hu	homeotic gene regulat	hypothetical protein	CD40 ligand - bovine	signal-transducing hi	beta-glucosidase homo	CD40 ligand - human	probable integrase -	hypothetical protein	lymphotoxin beta - hu	tumor necrosis factor
4.31e+00	4.31e+00	4.31e+00	4.31e+00	4.31e+00	3.24e+00	3.24e+00	2.43e+00		1.36e+00	1.36e+00	1.01e+00	1.01e+00	1.01e+00		5.57e-01	3.05e-01		2.25e-01	6.94e-03	9.00e-07	7.97e-1

RESULT 2	Db 187 HLHF Qy 158 LVDY	Db 127 YLAH :: Qy 99 SITV	Db 73 SLLW : Qy 39 ALHW	Query Match Best Local S Matches 5	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #Authors #Journal #title #cross-refere #accession ##molecule ##residues ##residues ##residues ##note COMMENT This ove GENETICS #Journal #Introns CLASSIFICATION KEYWORDS SUMMARY	
	HLHFS-PSTVFFGAFAL 202 : :: LVDYTKEDKTFFGAFLL 174	YLAHEVQLESSQYPFHVPLLSAQKSVYPGLQGPWVRSMYQGAVFLLSKGDQLSTHTDGIS 186 : : : : : : : : : : :	SLLWRANTDRAFLRHGFSLNNNSLLIPTSGLYFVYSQVVFSG-ES-CSP-R-A-IPT-PI 126:	Query Match 18.4%; Score 242; DB 2; Length 202; Best Local Similarity 36.5%; Pred. No. 8.30e-25; Matches 50; Conservative 22; Mismatches 57; Indels 8; Gaps 8;	tumor necrosis factor beta - rat # tumor necrosis factor beta - rat # formal_name Rattus norvegicus #common_name Norway rat 3-May-1994 #sequence_revision 03-May-1994 #text_change 8SSIONS JN0869 RENCE Kwon, J.; Chung, I.Y.; Benveniste, E.N. 10urnal Gene (1993) 132:227-236 title Cloning and sequence analysis of the rat tumor necrosis cross-references MUD:94040766 accession JN0869 ##molecule_type DNA ##residues	

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TITLE
ALTERNATE_NAMES
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#title Induction of tumor necrosis factor-alpha and beta
interferon-gamma mRNA by interleukin 2 in murine
lymphocytic cell lines.
#cross-references_MIID:89144562
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#journal Nucleic Acids Res. (1987) 15:9083-9084

#title Nucleotide sequence of the murine TNF locus, including

TNF-alpha-(tumor necrosis factor) and TNF-beta-
(lymphotoxin) genes.

#cross-references_MUID:88067722
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                                                                                                                  Li, C.
J. Immunol. (1987) 138:4496-4501
Cloning and expression of murine lymphotoxin cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N. Nucleic Acids Res. (1987) 15:3937
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The genes for tumor necrosis factor (TNF-alpha) and
                                                                                                                                                                                                                                                                                                                                                                                                  The murine tumor necrosis factor-beta (lymphotoxin) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the cloned genes, physical linkage, and chromosomal position.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weil, D.; Dautry,
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#introns 32/3; 66/1
SSIFICATION #superfamily tumor necrosis factor ASSIFICATION #superfamily tumor necrosis factor (Property of the Color of the
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m NT} The first intron occurs in the 5'-untranslated region.
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##cross-references GB:U06948; NID:g473564; PID:g473565
## #length 279 #molecular-weight 31442 #chec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 36.5%; res 50; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 SITVVITKVTDSYPEPTQLLMGTKSVC-EVGSNWFQPIYLGAMFSLQEGDKLMVNVSDIS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 SLLWRASTDRAFLRHGFSLSNNSLLIPTSGLYFVYSQVVFSG-ES-CSP-R-A-IPT-PI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 PYVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMT 82
                                                                                                                                                                                                                                                                                                                                                    SLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTK-SVCEVGSNWFQPIYLGAMF 141
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A53062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.;
Copeland, N.G.; Suda, T.; Nagata, S.
Cell (1994) 76:969-976
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                                                                        lymphotoxin; TNF beta
#formal_name Oryctolagus cuniculus #common_name domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Mus musculus #common_name house mouse
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
                                                                                                                                                     tumor necrosis
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                                                                                                                                                     factor beta precursor - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 232; DB 2;
Pred. No. 5.78e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.27e-24; 22; Mismatches 57
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Best Local S
Matches 4
                                                                                                                           #title Cytokine (1993) 5:336-341

#title Cloning and characterization of the tandemly an ecross-references MUID:94083525

#accession I46046
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                    Introns
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##cross-references GB:M60340; GB:M35326; NID:g165754; PID:g165755;
GB:M60341; GB:M35327; NID:g165757; PID:g165758
                                                        ##cross-references EMBL:Z14137;
                                                                                           ##molecule_type DNA
                                                                                                                   ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 YLAHEVQLFSSQYSFHVPLLSAQKSVCPGPQGPWVRSVYQGAVFLLTQGDQLSTHTDGIA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
##residues 1-197 ##label SHA
##cross-references GB:X55745; NID:g297167; PID:g297168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 17.4%;
Local Similarity 33.6%;
hes 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVDYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HL-LLSPSSVFFGAFAL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLRWRANTDRAFLRHGFSLSNNSLLVPSSGLYFVYSQVVFSG-EG-CSP-K-AV-PT-PL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily tumor necrosis factor
cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning and structural analysis of the genes, coding for rabbit tumor necrosis factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andreyeva, A.V.; Nedospasov, S.A. Mol. Biol. (Mosk.) (1989) 23:1743-1750
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Gene (1990) 95:215-221

Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis factor).
#superfamily tumor
                  32/3;
                                                                                                                                                                                                                                                   Cludts, I.; Cleuter, Y.; Kettmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25/3; 61/1
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                                                                                                                                                                                                                                                                                                                            #formal_name Bos primigenius taurus #common_name cattle 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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                                                                                                                                                                                                                                                                         I46046
                                                                                                                                                                                                                                                                                          I46046; S24641
                                                                                                                                                                                                                                                                                                                                                                 #type complete
lymphotoxin - bovine
                                                                                                                                                                                                                                                                                                              08-Nov-1996
                                                                           1-204 ##label CL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain signal sequence #status predicted #label SIG\
#product lymphotoxin #status predicted #label MAT
#th 197 #molecular-weight 21126 #checksum 8190
                                                                                                             preliminary; translated
                      68/1
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  necrosis factor
                                                        NID:g796;
                                                                                                                 from GB/EMBL/DDBJ
                                                        PID: g797
                                                                                                                                                                                                                                                   R.;
                                                                                                                                                                                                                                                 Burny, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.L.; Azizov, M.M.;
                                                                                                                                                                                          arranged boyine
                                                                                                                                                                        genes.
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Best Local Similarity 35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal Int. Immunol. (1994) 6:1567-1574
#title Human Fas ligand: gene structure.
species specificity.
#cross-references MUID:95127560
#gene
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#accession JC2340
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##residues 1-281 ##label MIT
##residues 3-281 ##label MIT
##residues 3-281:038122; DDBJ:D29820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references EMBL:Ul1821; NID:g595430; PID:g595431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
                                        ##cross-references EMBL:U08137;
                                                              ##residues
                                                                             ##molecule_type mRNA
                                                                                                     ##status
                                                                                                                                                                                                                                                                                                            ##cross-references EMBL:X89102; NID:g887455; PID:g887456
                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                              Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.
J. Exp. Med. (1995) 181:71-77
Fas ligand mediates activation-induced cell death in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Kamada, T. Biochem. Biophys. Res. Commun. (1994) 204:468-474
Role of Fas ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                S57565
                                                                                                                                                                                                                                                                                                                                                                                                               Schatzlein, C.E. submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formai_name Homo sapiens #common_name man
29-May-1998 #sequence_revision 29-May-1998 #text_change
03-Aug-1998
                                                                                                                        I38554
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Pred. No. 2.05e-22;
23; Mismatches 58;
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                                      NID:g624627;
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                                                                                                     from
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                                        PID: g624628
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34-204
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#journal Gene (1991) 102:171-178
#title The porcine tumor necrosis factor-encoding genes: sequence
and comparative analysis.
#cross-references_MUID:91340150
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                                                                                                                          158 LVDYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                  129 YLAHEVQLFSSQYPFHVPLLSAQKSVCPGPQGPWVRSVYQGAVFLLTQGDQLSTHTDGTP 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
##residnes 1-204 ##label KUH
                                                                                                                                                               189 HL-LLSPSSVFFGAFAL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:X54859; NID:g2132; PID:g2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
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                                                                                                                                                                                                                                                                                                                                                                                   Local
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Similarity 35.8%;
49; Conservative
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Similarity 32.8%;
45; Conservative
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#formal_name Rattus norvegicus #common_name
                    fas
                                                                                                                                                                                                                                                                                                                                                                                                                                             #length 204 #molecular-weight 21960 #checksum
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#product tumor necrosis factor beta #status predicted
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                                                                                                                                                                                                                                                                                                                                                              Score 217; DB 2;
Pred. No. 3.12e-20;
25; Mismatches 59
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Pred. No. 8.93e-21;
30; Mismatches 43
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                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 204;
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      Norway
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#accession A49266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakaguchi, A.Y.; Goeddel, D.V.; Gray, P.W.
#journal J. Cell. Biochem. (1985) 29:171-181
#title Structure and chromosomal localization of the human
lymphotoxin gene.
#cross-references_MUID:86086150
                                                                       #authors
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##cross-references GB:U03470; NID:g440178; PID:g440179
RDS glycoprotein; transmembrane protein
#length 278 #molecular-weight 31140 #checksum
                                                                                                                                          ##residues 1-12,'R',14-205 ##label IRI ##cross-references EMBL:Z15026; NID:g37211; PID:g37213 ##note the nucleotide sequence was submitted
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nes 50; Conservation
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Primas, G.; Perrot, V.; Jurka, J.; Rodriguez-Tome, P.;
Claverie, J.M.; Dausset, J.; Cohen, D.
Nature Genet. (1993) 3:337-145
Dense Alu clustering and a potential new member of the
NFkappaB family within a 90 kilobase HLA class III segment.
S36154
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Haplotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nedwin, G.E.; Jarrett-Nedwin, J.; Smith,
Sakaguchi, A.Y.; Goeddel, D.V.; Gray,
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Immunogenetics (1991) 33:50-53 Haplotypic polymorphisms of the
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lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF
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                                                                     Abraham, L.J.; Du, D.C.; Zahedi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Homo sapiens #common_name man
28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change
                                                  Whitehead,
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                                                                                                                                                                                                                                 nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1-59,'N',61-205 ##label NED
                                                                                                              Library, August 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 212; DB 2;
Pred. No. 2.48e-19;
28; Mismatches 44
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##cross-references GB:X01393; NID:g34444; PID:g344445
##experimental_source lymphoblastoid cell line RPMI-1788
NCE A32877
                                                                                 ##note
                                                                                                 ##molecule_type protein
##residues 35-59,'N',61-205 ##label VOI
                                                                                                                                                                                                                                                                                          ##molecule_type protein
56-79;86-95,'x',97,'X',99;119-151,'XX',154-162,'X',164,
'X',166,'X',168,'X',170,'X',172-173 ##label FUK
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1124,'p',126-205 ##label RES

##cross-references GB:M55913; NID:g339742; PID:g339743

##experimental_source ancestral haplotype 57.1

##note 59-Asn was also found (ancestral haplotype 8.1)
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                                                                                                                                                                            Natural human tumor necrosis factor beta (lymphotoxin).

Variable O-glycosylation at Thr(7), proteolytic processing, and allelic variation.
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Lymphokine Res. (1988) 7:175-185
Simultaneous production of natural human tumor necrosis
factor-alpha, beta and interferon-alpha from BALL-1 cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Henzel, W.J.; Jarrett, J.A.; Leung, D.W.; Moffat, B. P.; Svedersky, L.P.; Palladino, M.A.; Nedwin, G.E. Nature (1984) 312:721-724 Cloning and expression of cDNA for human lymphotoxin, lymphokine with tumour necrosis activity.
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                                            Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura,
                                                                                                                                                                                                                                       Voigt, C.G.; Maurer-Fogy, I. FEBS Lett. (1992) 314:85-88
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T.; Yamashita, K.
rch. Biochem. Biophys. (1993) 304:144-153
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                                                                                     60-Thr was also found
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                                                                                                                                                                                                                                                         I.; Adolf, G.R.
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Query Match 15.2%;
Best Local Similarity 31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 YLAHEVQLFSSQYPFHVPLLSSQKMYYPGLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIP 189
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                                                                                                                                     ##cross-references EMBL:X14828; NID:g992; PID:g993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITVVITKVTDSYPEPTQLLMGTKSVC-EVGSNWFQPIYLGAMFSLQEGDKLMVNVSDIS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted from mitogen-activated lymphocytes within 1-2 days after induction, this lymphotoxin can cause cytolysis of certain tumor cell lines and have an antiproliferative effect on others while having no detrimental effect on normal cells. It can also act synergistically with interferon gamma to kill certain transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   different induction kinetics.
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                                                                                 Rimstad,
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$06192
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28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
08-Sep-1997
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#title
                                                                         polymerase chain reaction and determination of the nucleotide sequence.
#cross-references_MUID:90034181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal Gene (1991) 102:171-178
#title The porcine tumor necrosis factor-encoding
#total and comparative analysis.
#cross-references_MUID:91340150
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##residues 1-232 ##label KUH
##cross-references EMBL.X54859; NID:g2132; PID:g2134
##note the authors translated the codon GAG
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125-144,'G',145-173,'L',175-193 ##label RIM
##cross-references EMBL:X77317; NID:g452607; PID:g452608
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Similarity 28.7%;
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                                                                                                                                                                                                                                                                                                                                                                                  S18965
Choi, C
                                                                                                                                       Pauli, U.; Beutler, B.; Peterhans, E. Gene (1989) 81:185-191
Porcine tumor necrosis factor alpha: Cloning with the
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Gene sequence of porcine tumor necrosis factor alpha.
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tumor necrosis factor alpha precursor - pig
#formal_name Sus scrofa domestica #common_name domestic
07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
08-Sep-1997
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44-232 ##label
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Pred. No. 1.75e-16;
31; Mismatches 60;
                                          from GB/EMBL/DDBJ
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Best Local
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.;
Jarrett-Nedwin, J.; Pennica, D.; Goeddel, D.V.; Gray, P.W.
#journal Nucleic Acids Res. (1985) 13:6361-6373
#title Human lymphotoxin and tumor necrosis factor genes: structure,
homology and chromosomal localization.
#cross-references MUID:86016093
                                       and homology to lymphotoxin #cross-references MUID:85086244
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##cross-references EMBL:Z15026; NID:g37211; PID:g37212
##note the nucleotide sequence was submitted to
Library, August 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-233 ##label NED 1-235; NID:g37209; PID:g37210
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##molecule_type mRNA
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Local Similarity 25.9%;
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                                                                                                                                                                                                                                                                                                                                                         Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.;
Prinas, G.; Perrot, V.; Jurka, J.; Rodriguez-Tome, P.;
Claverie, J.M.; Dausset, J.; Cohen, D.
Nature Genet. (1993) 3:137-145
Dense Alu clustering and a potential new member of the
NFkappaB family within a 90 kilobase HLA class III segment.
                                                                                                                         Pennica, D.; Nedwin, G.E.; Hayf. Derynck, R.; Palladino, M.A.; Goeddel, D.V.
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cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;
                      A93351
                                                                                 Nature (1984) 312:724-729
Human tumour necrosis factor:
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Pred. No. 1.75e-16;
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                                                                                                                                               Hayflick, J.S.; :
                                                                                 precursor structure,
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#title
##cross-references GDB:120441; OMIM:191160
#map_position 6p21.3-6p21.3
#introns 62/3; 78/1; 94/1
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                                                                                                                                                                                                                                                                    ##mollecule_type protein
##residues
77-99 ##label TAK
##residues
VIT Secreted from mitogen-activated macrophages within 4-24 hours after
induction, TNF-alpha can cause cytolysis of certain tumor cell
lines and have an antiproliferative effect on others without
detriment to normal cells. It can also act synergistically with
interferon gamma to kill certain transformed cell lines.
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##residues 83-102;109-119;121-128,'X',130-131;142-144,'X',146,
'XXX',150-152;159-174;180,'X',182-204 ##label FUK
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                                                                                                                                                              TNF-alpha and -beta (lymphotoxin) are the products of different genes closely linked on chromosome 6. They are induced by similar mitogenic stimuli and have similar biological activities but are produced by different cell types and have different induction
                                                                                                                                          kinetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M. Eur. J. Biochem. (1985) 152:515-522
Molecular cloning and expression of human tumor necrosis factor and comparison with mouse tumor nectosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, Eur. J. Biochem. (1996) 235:431-437 O-Glycosylated species of natural human tumor-necrosis factor-alpha.
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Lymphokine Res. (1988) 7:175-185
Simultaneous production of natural human tumor necrosis
factor-alpha, -beta and interferon-alpha from BALL-1 cells
stimulated by HVJ.
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Molecular Cloning of the complementary DNA for human tumor
                                                                                     GDB:TNF; TNFA
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this protein was isolated from the monocyte-like cell
line HL-60 from a promyelocytic leukemia
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(1985) 260:2345-2354
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Nedwin, G.E.;
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goe, K.;
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Goeddel,
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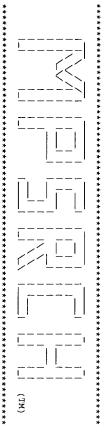
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Local Similarity 27.9%;
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                                  lymphotoxin-beta - mouse #formal_name Mus musculus #common_name house mouse 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_c
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cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;
I49139; I49138; I49076
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tumor necesis factor - baboon
#formal_name Papio sp. #common_name baboon
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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#label MAT\
                                                                                               #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 191; DB 2;
Pred. No. 1.32e-15;
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Pred. No. 3.93e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                SUMMARY
                                                                                              CLASSIFICATION
                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                        ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.5%;
Best Local Similarity 26.9%;
Matches 39; Conservative
    Query Match
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#title
                                                                                                                                                                                                           #authors Young, A.J.; Hay, J.B.; Chan, J.Y.C.
#journal Nucleic Acids Res. (1990) 18:6723
#title Primary structure of ovine tumor necrosis factor alpha cDNA.
#cross-references MUID:91067496
#accession S13114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #introns
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#title Characterization of the mouse lymphotoxin-beta gene.
#cross-references_MUID:95088371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #gene
                                                                                                                                              ##molecule_type DNA
##residnor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 GLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPP-AG-R-S-RA-RS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status preliminary
##molbecule_type DNA
##residues 1-306 ##label RE2
##cross-references EMBL:U12029; NID:g515508; PID:g515509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
##residues 1-306 ##label RE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 MVNVSDISLVDYTKEDKTFFGAFLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 YVNISHPDMVDYRR-GKTFFGAVMV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 LTLRSALYRAĞGAYGRGSPELLLEGAETVTPVVDPIGYGSLMYTSVGFGGLAQLRSGERV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references EMBL:U16984; NID:g577431; PID:g577432
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                                                            ##residues 1.23 ##label YOU
##cross-references EMBL:X55966; NID:g1403; PID:g1404
#FICATION #superfamily tumor necrosis factor
DS transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 DSITVVITKVTDSY-PEPTQLLM-G--T-KSVCE-VG-SN-WFQPIYLGAMFSLQEGDKL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 ALHWEHELGLAFTKNRMNYTNKF-LLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pokholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov, S.V.; Novobrantseva, T.I.; Turetskaya, R.L.; Green, J.E.; Nedospasov, S.A. Proc. Natl. Acad. Sci. U.S.A. (1995) 92:674-678 Cloning and expression analysis of the murine lymphotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149138
                                                                                                                                                                                                                                                                                                                                                                                            $13114  #type complete
tumor necrosis factor alpha - sheep
#formal_name Ovis orientalis aries, Ovis ammon aries
#common_name domestic sheep
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT-beta
54/3; 160/1
#length 306 #molecular-weight 32328 #checksum 6433
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                                                #length 233
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    14.48;
                                                #molecular-weight 25408 #checksum 7786
    Score 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 191; DB 2; Length 306; Pred, No. 1.32e-15; 45; Mismatches 46; Indels 15;
    DB 2;
Length 233;
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Matches 39; Conservative
  159 VDYTKEDKTFFGAFLL 174
                                     218 LDYAESGQVYFGIIAL 233
                                                                                 100 ITVVI-TKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISL 158
                                                                                                                           159 IAVSYQTKVNILSAIKSPCHRETLEGAE-AKPWYEPIYQGGVFQLEKGDRLSAEINLPEY 217
                                                                                                                                                                                                            102 LRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRG-HG-CPSTPLF-LTHTISR 158
                                                                                                                                                                     40 LHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDS 99
                                                                                                                                                                                                                                                      Pred. No. 2.94e-15; 30; Mismatches 62;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                      Gaps
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Search completed: Tue Jan $18\ 13:20:11\ 2000$ Job time : $24\ \text{secs}$.



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MPsrch_pp protein protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 18 13:18:22 2000; MasPar time 14.38 Seconds 257.319 Million cell updates/sec

Tabular output not generated

(1-174) from US09246129A.pep 1314 >US-09-246-129-2

Description: Perfect Score: Sequence: MRRFLSKVYSFPMRKLILFL......DISLVDYTKEDKTFFGAFLL 174

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Statistics: Mean 31.581; Variance 131.813; scale 0.240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	₽B	ID .	Description	Pred. No.
ъ	1301	99.0	174	18	R99453	Tumour necrosis facto	8.21e-118
2	252	19.2	169	25	W25079	۲.	2.66e-13
ω	247	18.8		23	W10875		7.76e-13
4	243	18.5		w	P50056	Sequence of murine ly	1.82e-12
ر ت	241	18.3		œ	R41866	Murine TNF-beta mutei	2.79e-12
0	238	18.1		N	R06359	TNF analogue.	5.28e-12
7	237	18.0		30	W40364	Rat Fas ligand-like p	6.53e-12
80	235	17.9		31	W56762	Murine TRAIL polypept	9.98e-12
9	235	17.9	291	23	W19788	Mouse apoptosis induc	9.98e-12
10	235	17.9		29	W44353	Murine AGP-1.	9.98e-12
11	232	17.7		14	R79067	Mouse Fas ligand (par	1.88e-11
12	232	17.7		14	R79068	Mouse Fas ligand (par	1.88e-11
13	232	17.7		14	R79069		1.88e-11
. 14	232	17.7		14	R79098	•	1.88e-11
15	231	17.6	279	36	W76332	Human TL2 (TRAIL), li	2.33e-11
16	231	17.6	279	18	R88357	Mouse Fas ligand.	2.33e-11

Query Match
Best Local Similarity
Matches 173; Conser

99.0%; ilarity 99.4%; Conservative

0;

Mismatches

0;

Gaps

0

Score 1301; DB 18; Pred. No. 8.21e-118;

Length 174; Indels

4.5	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	1/
220	N	N	N	N	N	N	N	N	N	\sim	N	\sim	\sim	Ν	\sim	2	Ν	N	N	2	\sim	\sim	ω	w	ω	ω	w	u
16.7		6	5	6	5	5	6	6	σ.	6.	σ.	6.	6	σ.	σ.	5	6.	6.	7.	7.	7.	7.	7.	7.	7.	7.	7 .	`.
287 26	81 3	81 1	81 1	81 1	81 2	81 1	68 3	65 3	79 1	51 2	41 1	39 1	38 1	38 1	37 1	36 1	36 3	30 1	39 3	05	71	57 2	81 2	81 3	81 3	81 2	81 2	7 78
Σ:	W7595	R7728	R7909	R8835	W2714	R9810	W4895	W4895	R7909	W1666	R8830	R8830	R7906	R8830	R7910	R8830	W4895	R7909	W4036	R2366	R4186	W108	W4435	W7682	W5676	W197	W197	W 2 / 1
Fas ligar	n Fas ligand.	S-L	s lig	s lig	Human Fas ligand.	s ligand der	able Fa	Fas li	gand (pa	Ω	ally delete	ally delet	s ligand (p	ally delet	Human Fas ligand (par	N-terminally deleted	Fas ligand fragment (Fas lig	Ovine TNF-beta.	ca mut	TNFL/LT-alpha hybrid.	Human AGP-1.		Human TRAIL polypepti		Novel cytokine Apo-2	Human Apoptosis induc
2.37e-10	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.37e-	.28e-	.56e-	.56e-	.39e-	.33e-	.33e-	.33e-	.33e-	.33e-	. 33

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RESULT
AC RAS
AC
                                                                Claim 1; Fig 1: 69pp; English.

Human tumour necrosis factor-gamma (R99453) is a novel member of the TNF family. It is encoded by a cDNA clone (T30390) isolated from a human umbilical vein endothelial cell cDNA library.

Recombinant TNF-gamma can be expressed in bacterial, insect or mammalian cells transformed with a vector carrying the TNF-gamma coding sequence. It is used to inhibit tumour cell growth, to provide resistance to infection, to induce inflammatory activity, for wound healing etc., and to screen for (ant)agonists or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor-gamma. TNF-gamma; cancer; tumour; gene therapy; wound healing.
        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor gamma and corresponding DNA and RNA - for treating cancer, facilitating wound healing and providing resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
Ni J, Rosen CA, Yu G;
WPI; 96-321550/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1994;
07-NOV-1994;
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17-MAY-1996.
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R99453;
14-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               against infection
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                                               raise antibodies.
        174 AA;
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; WO-U12880.
; ZA-009229.
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26..174
/label= Mat_protein
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RESULT
ID W
AC W
AC W
DT 25
DE FE
KW C
KW C
KW S
KW S
OS S
FH KW KW
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Best Local
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W10875 stand
W10875;
25-SEP-1997
                                                                 Fast/LT-alpha hybrid. C-terminal extracellular domain; CD40 ligand; mutated; trimerisation; Cymphotoxin; LT; beta; alpha; tumour necrosis factor; TNF; inhibitor; signalling; receptor; Fas; treating; autoimmune disease; diabetes; rheumatoid arthritis; inflammatory bowel disease; HIV proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence comprises a new peptide inhibitor of cancer metastas animals. The inhibitor has a generic sequence: X'-X (I); (the amin sequence of the fourth circumscribed portion of TMF-alpha), where hydrogen or a polypeptide of any size; and X'- a polypeptide of 1-residues, preferably as above, with the proviso that X-X' is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mizuno
WPI; 97
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W25079;
  Synthetic.
Key
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TNF-alpha; tumour metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
CN1101572-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Met-Val-Arg-Ser-Ser-Arg-Thr-Pro-Ser-Asp-Lys-Pro-Val-Ala-His-Val-Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page -; 11pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour metastasis-suppressing agent - especially for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1993; 115007.
15-OCT-1993; CN-115007
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                                                immune response; tissue graft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    veterinary medicine
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Wizuno D, Soma
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19..169
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1..18
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 252; DB 25;
Pred. No. 2.66e-13;
37; Mismatches 54
                                                                                                                                                                                                                                                                                                                                            174
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PT Heteromeric complexes comprising lymphotoxin sub-units - useful as prinhibitors of signalling by TNF- and TNF-related receptors, for treating auto:immune disease, graft rejection. etc.

PT treating auto:immune disease, graft rejection. etc.

PS Disclosure; Fig 10; 87pp; English.

CC This sequence comprises the C-terminal extracellular domain of the Fas CC ligand altered to drive trimerisation with wild-type lymphotoxin (LT)-cc beta. LT subunit association domains potentiate subunit associations into an active trimeric ligand. Tumour necrosis factor (TNF)-related ligand CC an active trimeric ligand. Tumour necrosis factor (TNF)-related ligand CC monomers mutated in their respective subunit associations domains can CC form heteromeric complexes with LT subunits. LT-alpha/beta heteromeric CC complexes and LT heterotrimeric complexes are useful as inhibitors of CC signalling by TNF receptors (R) and TNF-related receptors, such as CD40, CC signalling by TNF receptors. By inhibiting TNF-residentling the complexes CC including diabetes, rheumatoid arthritis, inflammatory bowel disease and CC including diabetes, rheumatoid arthritis, inflammatory bowel disease and CC including diabetes, rheumatoid arthritis, inflammatory bowel disease and CC are also useful for preventing or reducing the severity of an immune CC semence 180 AB.
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misc_difference 139
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WPI; 97-087055/08
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07-JUN-1995; US-476074.
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                                       slvnf-eesttffgafkl 180
                                                                                                    ---vym-r-nskypqdlvllssxkmvycttgqmwahssylgaafnlttsadhlyvnvsel 163
                                                                                                                                                              ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD
SLVDYTKEDKTFFGAFLL
                                                                             SITVVITKVTDSYPEPTQLLMGTKSV-CEVGSNWFQPIYLGAMFSLQ-EGDKLMVNVSDI 156
                                                                                                                                                                                                                                            Conservative
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174
                                                                                                                                                                                                                                                               Score 247; DB 23; Pred. No. 7.76e-13;
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Matches 5
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Example; Fig 4; 29pp; English.
The inventors claim new pure lymphotoxin and its derivs. for antitumour use. The variants are esp. lymphotoxin wherein an AA residue in the SQ in P50055 has been (a) deleted, (b) substituted another residue (c) another residue has been inserted into the SQ provided, however, that such variant lymphotoxin excludes having amino terminii at Leu(35) or His(57). Nucleic acids encoding such a such control of the square of the squa
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EP-164965-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1985; 119648.
31-MAY-1984; US-616502.
31-MAY-1984; US-616503.
09-MAY-1985; US-732312.
                                                                                                                                                                                                                                                                                                                                                                                                 Murine TNF-beta mutein with modified channel-forming activity. Tumour Necrosis Factor beta; TNF-b; target membrane permeability; TNF trimer; ion channel; mutein; planar lipid membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peduence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antitumour agent; tumour necrosis factor.
                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                             R41866;
29-MAR-1994
                                         misc_difference
                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R41866 standard; protein; 169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L8-DEC-1985.
                                                                                                                                                                                                                                                                                                                                                                                  lymphotoxin; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ymphotoxins are also claimed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ylahevqlfssqypfhvpllsaqksvypglqgpwvrsmyqgavfllskgdqlsthtdgis 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENENTECH INC. GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
32..200
                                       /note= "wild-type channel residue is Lys" 125
                                                                                                                        /note=
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                           /note= "wild-type channel residue is
    /label= Arg,
or His
                                                                                                                                                                                                   /label= Trp, Ser,
/note= "wild-type
                                                                                               /label= Arg, Cys,
                                                                                                                                                              'label=
                                                                                                                                                                                                                                                                                                 label= Glu, Arg,
                                                                                                                                     = Trp, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pre-region
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Pred.
23; M
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. No. 1.82e-12;
Mismatches 56;
                                                                                                                                                                                                                      Thr,
                                                                                                                                                                                                                                                                                                 Cys,
                      Asp,
                                                                                                   Glu,
                                                                                                                                                            Thr,
                                                                                                                                                                                                   channel
                                                                                                                                           channel
                                                                                                                                                                                                                      Ala,
                      Gln,
                                                                                                                                                            Ala,
                                                                                                                                                                                                                                                                                                     Asp,
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                                                                                                                                           residue
                                                                                                                                                                                                   residue
                    Asn,
                                                                                                 Gln,
                                                                                                                                                                                                                      Met,
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                                                                                                                                                                                                                    Cys,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
10-JUL-1990.
28-DEC-1988; 328852.
28-DEC-1988; JP-328852.
(TEIJ ) TEIJIN KK.
WPI; 90-252060/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the corresp. position \mbox{misc\_difference} 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 45 and 63-65; 72pp; English.
The sequence of murine lymphotoxin (TNF-beta) disclosed
J.Immunology 138:4496-4501 (1987) is given in the specification.
A modified version of this sequence is claimed in which at least
of the channel residues is substituted (see Features Table). The
resulting TNF-beta mutein has modified channel activity compared
wild-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing modified tumour necrosis factor alpha - uregulating tumour necrosis factor channel activity increasing permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference
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WPI; 93-30346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1993.
12-MAR-1993; U02475.
12-MAR-1992; US-852625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                           J02177896-A.
                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                        TNF analogue
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                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 ylahevqlfssqypfhvpllsaqksvypglqgpwvrsmyqgavfllskgdqlsthtdgis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93-303462/38
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                                                                                                                                                                                                                      necrosis
                                                                                                                                                                                                                                                                                                        standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 50; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AA;
                                                                                                                                                                                                                                                               (first entry)
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mote= "wild-type 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "wild-type 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or Thr
/note= "wild-type
human lymphotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "wild-type 167
                                                                                                                                                                                                                      factor; tumouricide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the corresp. position
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human lymphotoxin the amino acid residue a
                                                                                                                                                                          Location/Qualifiers
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/note= "wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Lys, Cys,
                                                                                                                                    /label=F or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                                                                                                                                                                                                            157
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22; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 241; DB 8;
Pred. No. 2.79e-12;
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                                                                                                                                                                                                                                                                                                            ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               channel residue
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nel residue is Tyr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is Phe"
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                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9803648-A1.
29-JAN 1998.
17-JUL-1997; J02480.
31-JAN 1997; JP-019330.
19-JUL-1996; JP-191204.
09-AUG-1996; JP-211695.
                                                                                                                                                                                                                         This sequence represents a novel rat Fas ligand-like protein. This protein can be used as a therapeutic and/or prophylactic agent for cancer, viral infection, Helicobacter pylori infection, invasive staphylococcia, hepatitis, nephritis, bone disease, atherosclerosis or pain. The protein can also be used in a method to treat acquired immune deficiency syndrome (AIDS), joint tissues in rheumatism, inflammation, hepatitis, neurodegenerative disease due to osteomyelodysplasia, ischaemic disease, autoimmune disease, diabette complications, ischaemic disease, autoimmune disease, diabettes, diabettic complications, and cardiomyopathy, influenza, glomerulonephritis or ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                               Pas ligand-like protein with apoptosis inducing activity - useful as therapeutic or prophylactic agent for cancer, viral infection, Helicobacter pylori infection, invasive staphylococcia, hepatitis, nephritis, bone disease, atherosclerosis or pain Claim 1; Page 167-168; 120pp; English.
                                                                                                                                                                                                                cardiomyopathy,
Sequence 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Fas ligand-like protein.

Fas antigen; ligand-like; apoptosis-inducing activity; therapeutic; prophylactic; cancer; viral infection; hepatitis; nephritis; influenza; bone disease; atherosclerosis; inflammation; neurodegenerative disease; ischaemic disease; autoimmune disease; diabetes; cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physiologically active polypeptide(s) - have defined sequence of 150 amino acid residues and are useful as tumouricides Claim 1; Page 1; 10pp; Japanese. The protein is produced by modification of a TNF expression plasmid. A Met residue is optionally bonded to the N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAKE ) TAKEDA CHEM IND LTD.
Hikichi Y, Nishi K, Shintani Y;
WPI; 98-120773/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uz-JUL-1998 (first
Rat Fas ligand-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; V10664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ulcerative colitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
SITVVITKVTDSYPEPTQLLMGTKSVCE-VGSN--WFQPIYLGAMFSLQEGDKLMVNVSD
                            pithglykrtsrypkelellvsrrspcgranssrvwwdssflggvvhleageevvvrvpg 220
                                                                    ALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPD
                                                                                      inrpdyldfaesgqvyfgiixf 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITVVITKVTDSYPEPTQLLMGTKSVC--EV--GSN---WFQPIYLGAMFSLQEGDKLMVN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                           Similarity
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                                                                                                                                           18.0%;
larity 32.4%;
Conservative
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                                                                                                                                           Pred.
36; 1
                                                                                                                                                         Score 237; DB 30;
Pred. No. 6.53e-12;
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Pred. No. 5.
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.28e-12;
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Best Local
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29-JUN-1995; US-496632.
01-NOV-1995; US-548368.
(IMMV) IMMUNEX CORP.
GOODWIN RG, WILLEY SR;
WPI; 98-347322/30.
N-PSDB; V29520
                                                              Tumour necrosis factor related apoptosis inducing ligand; TRAIL; cytokine; cancer; leukaemia; lyphoma; melanoma; viral infection; thrombotic microangioplasty; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections Claim 1; Columns 41-44; 28pp; English.

This represents a murine tumour necrosis factor related apoptosis ligand (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful in studies of Jurkat cells. The encoding nucleic acid sequences are useful in studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells (e.g. to isolate antigens for vaccine development). The polypeptides can be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal treatment of blood or bone-marrow), or to treat viral infections.
                                                     Mus musculus.
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Tumour necrosis factor related apoptosis ligand; TRAIL;
Tumour necrosis factor related apoptosis ligand; viral
                                                                                                                                                              Mouse apoptosis
                                                                                                                                                                                                                                             W19788 standard; Protein; 291
                                                                                                                                                                                          24-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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25-JUN-1996; 670354.
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Similarity 31.48;
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18..38
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No. 9.98e-12;
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infection;
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domain

/label= Cytoplasmic_domain 18..38 /label= Transmembrane_domain

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected cells - useful for treating thrombotic microangiopathy, cancer and viral infection and for use in assays Claim 10: Page 48.49; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse tumour necrosis factor related apoptosis inducing ligand (TRAIL) (W19788) is a novel cytokine that induces apoptosis of certain target cells, including cancer cells and virally infected cells. Its amino acid sequence was deduced from CDNA clone MUAIC (T72849), isolated from a T cell line 789 library. Human TRAIL (W19787) has also been identified. Recombinant TRAIL polypeptides (esp. soluble polypeptides) can be expressed in host cells and used the composition of the composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1995; US-496632.
01-NOV-1995; US-548368.
(IMMV) IMMUNEX CORP.
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06-JUN-1997; U09895.
07-JUN-1996; US-660562.
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protein
                         Nucleic
                                                  N-PSDB; V15294.
                                                                                             (AMGE-) AMGEN INC.
Danilenko DM, Johnson MJ,
                                                                                                                                                                                                                  Mus sp.
W09746686-A2.
                                                                                                                                                                                                                                                                                                                                                                                       W44353 standard; Protein; 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodwin RG,
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                                                                                                                                                                                                                                                                                                                  Murine AGP-1.
                                                                                                                                                                                                                                                                                                                                            28-MAY-1998
                                                                                                                                                                                                                                                                     inflammation;
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29-JUN-1995;
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Local Similarity 31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lmdldqea-sffgafli 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITVVITKVTDSYPEPTQLLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLMVNVSDIS 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEHEL-GLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPN-KPDS 99
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                                                                         98-042194/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVDYTKEDKTFFGAFLL 174
                         acid encoding AGP-1,
                                                                                                                                                                                                                                                                                              AGP-1; tumour necrosis
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  useful
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                                                                                                                                                                                                                                                                  ; tumour necrosis factor-related protein; bone resorption; haematopoietic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
162..1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
for treating inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "potential KEX2 protease processing site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extracelular_domain
                                                                                                Simonet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 235; DB 2
Pred. No. 9.98e:
35; Mismatches
                         a tumour necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235; DB 23;
No. 9.98e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEX2 protease
                                                                                                SM
  bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
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resorption and
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Best Local
      Matches
                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1994; JP-074344.
08-JUL-1994; JP-180955.
07-SEP-1994; JP-239363.
18-OCT-1994; JP-278378.
(MOCH ) MOCHIDA PHARM CO LTD.
(OSAB-) OSAKA BIOSCIENCE INST.
Nagata S, Nakamura N, Suda T,
WPI: 95-194031/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.

W09513293-A1.

18-MAY-1995.

10-NOV-1994; J01899.

10-NOV-1993; JP-305975.

13-DEC-1993; JP-342526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haematopoietic diseases
Claim 7: Page 33-34; 54pp; English.
Claim 7: Page 33-34; 54pp; English.
The present sequence represents murine AGP-1. AGP-1 is a tumour-necrosis factor (TNF)-related protein, involved in inflammation, myelopoiesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay reagents for detecting AGP-1 expression. Nucleic acid complementary to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation) or bone resorption diseases (e.g. osteoporosis, osteomyelitis, hypercalcaemia, Paget's disease). AGP-1 can be used to creat haematopoietic diseases associated with reduction in the number of bone marrow cells, particularly neutrophils and lymphocytes, e.g. where caused by disease, injury or exposure to myelosuppressive agents. Host cells, transformed with expression vectors containing AGP-1 DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus erythematosus, psoriasis, scleroderma, infection-related
                                                                                                                                                                                              Fas ligands or active fragments able to induce apoptosis in cells which express the Fas cell surface antigen are claimed. The proteins are isolated from human, rat and mouse sources. The present
                                                                                                                                                                                                                                                                                            N-PSDB: 099496.

Peptide which binds to Fas antigen, and antibody reactive with it for treatment and diagnosis of viral or auto:immune diseases Claim 9; Page 219-221; 300pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse Fas ligand (partial sequence). Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R79067;
22-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are used to produce recombinant AGP-1. Sequence 291 AA;
                                                                                                                                   sequence represents part of the mouse Fas ligand Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R79067 standard; Protein; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fas cell surface antigen; Fas-L; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 wessrkghsfl-nhvlfrngelviegeglyyiysqtyfrfgeae-daskmvskdkvrtkg 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 lmdldgea-sffgafli 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 LVDYTKEDKTFFGAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 lvqyiykyt-sypdpivlmksarnscwsrdaeyglysiyqgglfelkkndrifvsvtneh 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watch 17.9%; Local Similarity 31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 WEHEL-GLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPN-KPDS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITVVITKVTDSYPEPTQLLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLMVNVSDIS
Similarity
54; Conserv
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      Conservative
                                  17.7%;
35.3%;
Score 232;
Pred. No. 1.
32; Mismatc
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Pred. No. 9.98e-12;
35; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Т,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi T;
          Mismatches
                                      DB 14;
.88e-11;
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      50;
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                                                                     Length 137;
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      Gaps
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ID R7
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AC R7
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KW F8
KW F8
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Best Local S
Matches 5
       18-mAY-1995.

10-NOV-1994; J01899.

10-NOV-1993; JP-305975.

13-DEC-1993; JP-342526.
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10-NOV-1993; JP-305975.
13-DEC-1993; JP-342526.
13-DEC-1994; JP-074344.
18-MAR-1994; JP-180955.
07-SEP-1994; JP-278378.
18-OCT-1994; JP-278378.
                                                                                                                                                                                     Mouse Fas li
Fas ligand;
                                                                                                                                                                                                                               R79069;
22-FEB-1996 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOCH) MOCHIDA PHARM CO LTD.

(OSAB-) OSAKA BIOSCIENCE INST.

Nagata S. Nakamura N. Suda T. Takahashi T;

WPI; 95-194031/25.

WPSIDB; 099497.

Peptide which binds to Fas antigen, and antibody reactive with it for treatment and diagnosis of viral or auto:immune diseases Claim 10; Page 221-222; 300pp; Japanese.

Fas ligands or active fragments able to induce apoptosis in cells which express the Fas cell surface antigen are claimed. The proteins are isolated from human, rat and mouse sources. The prese sequence represents part of the mouse Fas ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas ligand; Tumour Necrosis factor family; apoptosis; cell death; Fas cell surface antigen; Fas-L; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R79068;
                                                                                                                                                                                                                                                                                            R79069
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18-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.7%;
Local Similarity 35.3%;
les 54; Conservation
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                                                                                                                                   cell surface antigen; Fas-L; mouse.
musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECSETROAGRPNKPDSITVVITKVTDSYPEPTQLLMGTK-SVCEVGSNWFQPIYLGAMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s-cnn--q---p--lnh-kvym-r-nskypedlvlmeekrlnycttgqiwahssylgavf 106
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                                                                                                                                                                                                                Fas ligand
                                                                                                                                                                                                                                                                                       standard; Protein;
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                                                                                                                                                                                   irst entry)
1 (partial se
pur Necrosis
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                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                     sequence)
is factor
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Pred.
32; M
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No. 1.88e-11;
                                                                                                                                                                                family; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                           174
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Best Local Similarity ?
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(OSAB-) OSAKA BIOSCIENCE I.
Nagata S. Nakamura N. Su
WPI: 95-194031/25.
N-PSDB; Q94156, Q99499.
                                                                                                                         10-NOV-1993; JP-305975.

13-DEC-1993; JP-342526.

18-MAR-1994; JP-074344.

08-JUL-1994; JP-180955.

07-SEP-1994; JP-239363.

18-OCT-1994; JP-278378.
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N-PSDB; 29498.

N-PSDB; 29498.

N-PSDB; 29498.

To treatment and diagnosis of viral or auto:immune diseases Claim 11; Page 222-224; 300pp; Japanese.

Fas ligands or active fragments able to induce apoptosis in cel which express the Fas cell surface antigen are claimed. The proteins are isolated from human, rat and mouse sources. The proteins are represents part of the mouse Fas ligand.

Sequence 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fas ligand; Tumour Necros: Fas cell surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 14
R79098 standard;
                                                                                                                                                                                                                                                                               18-MAY-1995.
10-NOV-1994; J01899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Fas ligand
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(OSAB-) OSAKA BIOSCIENCE INST
Nagata S, Nakamura N, Suda 1
WPI; 95-194031/25.
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08-JUL-1994; JP-180955.
07-SEP-1994; JP-239363.
18-OCT-1994; JP-278378.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTK-SVCEVGSNWFQPIYLGAMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour Necrosis factor family; apoptosis; cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                           258
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
117
                                                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= proline-rich 79..100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N-glycosylation_site
131
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= transmembrane_anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%;
                                                    Suda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 232; DB 14;
Pred. No. 1.88e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse.
                                                    Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi T;
                                                    H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                      ps Disclosure; Page 17-18; 22pp; English.

This is the amino acid sequence of human TL2 (also known as TRAIL), which has newly been discovered to be a ligand of human tumour necrosis related receptor TR5 (see W76331). This TR5 polypeptide of the invention and TL2 can be used in screening processes for compounds which bind the receptor, or its ligand, and which activate (agonists) or inhibit (antagonists) the receptor or TL2. Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist to the polypeptide administering a nucleic acid that inhibits the expression of the nucleotide sequence encoding the polypeptide and/or administering a polypeptide that competes with the polypeptide for its ligand, substrate or receptor. The active agents can be used for the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, procession of the active ischemia, autoimmune diseases (e.g. inflammatory bowel disease, attractive ischemia active restrictory disease syndrome restraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                             prevent and treat e.g. inflammation, arthritis, septicaemi autoimmune diseases, infections, stroke, ischeemia, ARDS, restenosis, brain injury, AIDS and bone diseases Disclosure; Page 17-18; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.45 ... apoptosis in cerrange 279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A clone (Q94156) contg. an insert coding for the mouse Fas ligand was isolated using probes derived from a rat Fas-L clone (see Q94153). The mouse sequence contains an open reading frame coding for a 279 amino acid sequence with 5 N-glycoslation sites and a proline-rich region. The deduced mouse amino acid sequence has 91.4% homology with rat Fas-L. Fas ligands are able to induce apoptosis in cells which express the Fas cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis; septicaemia; transplant rejection; autoimmune disease; inflammatory bowel disease; graft versus host disease; infection; stroke; ischaemia: acute respiratory disease syndrome; psoriasis; restenosis; brain injury; AIDS; bone disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-1999 (first entry)
Human TL2 (TRAIL), ligand for TR5.
TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which binds to Fas antigen, and antibody reactive with it for treatment and diagnosis of viral or auto:immune diseases Claim 12; Fig 23-24; 300pp; Japanese.
A clone (094156) contg. an insert coding for the mouse Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyn SDP, Tan KB, 'WPI; 98-497862/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-1997;
(SMIK ) SMITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-1998;
28-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-867509-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis; Alzheimer's disease; human; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W76332 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide encoding TR5 polypeptide - used to diagnose,
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hes 54; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s-cnn--q---p--lnh-kvym-r-nskypedlvlmeekrlnycttgqiwahssylgavf 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-1997; US-901469.
B-1997; US-795910.
) SMITHKLINE BEECHAM CORP.
                    injury,
ischaemia, acute respiratory disease syndrome, restenosis, njury, AIDS, bone diseases, cancer (e.g. lymphoproliferativers), atherosclerosis and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tan KB, Truneh
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35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation, arthritis, septicaemia
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32; №
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Pred. No. 1.88e-11
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                      lymphoproliferative
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 159
                                                      101 TVVITKVTDSYPEPTQLLMGTKSVC-EVGSNW-FQPIYLGAMFSLQEGDKLMVNVSDISL
                                                                                206
                                                                                                                         152 wessrsghsflsn-lhlrngelvihekgfyyiysqtyfr-fq-e--eikentkndk-qmv 205
                                                                                                           42
                                                                                                                                                                          Local Similarity
VDYTKEDKTFFGAFLL
                           id-mdheasffgaflv 278
                                                                              qy-iykyt-sypdpillmksarnscwskdaeyglysiyqggifelkendrifvsvtnehl
                                                                                                           WEHEL-GLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSI 100
                                                                                                                                                             47;
                                                                                                                                                                                                                  279
                                                                                                                                                               Conservative
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34.6%;
  174
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33; 1
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                                                                                                                                                             Mismatches 44;
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